

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:57:23 ; Search time 76.7143 Seconds
(without alignments)
34.365 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPVI 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	2	AAW77197
2	29	100.0	6	5	ABG78133
3	29	100.0	6	5	ABG91824
4	29	100.0	6	8	ADI28369
5	29	100.0	6	8	ADJ57364
6	29	100.0	6	8	ADJ57364
7	29	100.0	6	8	ADJ57364
8	29	100.0	6	9	ADJ57364
9	29	100.0	6	9	ADJ57364
10	29	100.0	246	5	ABG78329
11	29	100.0	246	5	ABG78329
12	29	100.0	256	5	ABG78334
13	29	100.0	256	5	ABG92025
14	29	100.0	266	5	ABG92020
15	29	100.0	277	5	ABG78150
16	29	100.0	277	5	ABG78150
17	29	100.0	277	8	ADI28366
18	29	100.0	277	8	ADI28366
19	29	100.0	278	8	ADI28367
20	29	100.0	278	8	ADI28367
21	29	100.0	280	8	ADI28368
22	29	100.0	280	8	ADI28368
23	29	100.0	280	8	ADI28368
24	29	100.0	280	8	ADI28368

25	29	100.0	442	8	ADN25218
26	29	100.0	464	5	ABG78151
27	29	100.0	464	5	ABG92021
28	29	100.0	464	5	ABG91842
29	28	96.6	133	4	AAU42688
30	28	96.6	133	6	ABM39207
31	28	96.6	438	5	AAE14569
32	28	96.6	438	7	ADA13449
33	28	96.6	438	7	ADA13415
34	28	96.6	438	7	ADG47134
35	28	96.6	438	7	ADG47100
36	28	96.6	470	7	ADA13459
37	28	96.6	470	7	ADG47144
38	28	96.6	541	4	AAO90242
39	28	96.6	973	7	ABO75198
40	27	93.1	116	6	AAU44808
41	27	93.1	116	6	ABM41327
42	27	93.1	152	9	AEBS4740
43	26	89.7	33	4	AAW82945
44	26	89.7	58	4	AAU56719
45	26	89.7	58	6	ABM53238
46	26	89.7	226	5	ABP73581
47	26	89.7	286	4	AGG98915
48	26	89.7	286	6	ABU15252
49	26	89.7	286	8	ADJ45133
50	26	89.7	289	8	ADY13333
51	26	89.7	290	6	ABU28269
52	26	89.7	319	8	ADX92867
53	26	89.7	350	2	ADY35225
54	26	89.7	405	7	ADC87283
55	26	89.7	477	7	ABO62389
56	26	89.7	514	7	ADX91171
57	26	89.7	530	8	ADY04822
58	26	89.7	1449	4	ABE66060
59	25	86.2	18	8	ADK01781
60	25	86.2	18	8	ADN48220
61	25	86.2	18	9	ADZ67861
62	25	86.2	18	9	ADZ67863
63	25	86.2	18	9	ADZ67864
64	25	86.2	18	9	ADZ67862
65	25	86.2	21	2	AAV12754
66	25	86.2	49	8	ADS06874
67	25	86.2	49	8	ADS07022
68	25	86.2	49	8	ADS04516
69	25	86.2	74	7	ADI60240
70	25	86.2	82	5	ABP08294
71	25	86.2	86	3	AGG18780
72	25	86.2	86	3	AAW90282
73	25	86.2	89	3	AAO28861
74	25	86.2	102	6	ABM65637
75	25	86.2	116	5	ABP32292
76	25	86.2	119	7	ABO79679
77	25	86.2	120	7	ADC97061
78	25	86.2	125	2	AAV11311
79	25	86.2	134	6	AAU45601
80	25	86.2	158	4	AAU42587
81	25	86.2	158	6	ABM39106
82	25	86.2	166	8	ADT57210
83	25	86.2	167	4	AAU56128
84	25	86.2	167	6	ABM52647
85	25	86.2	167	9	ABM93814
86	25	86.2	222	3	AAV84827
87	25	86.2	222	7	ABO61727
88	25	86.2	222	7	ADT87198
89	25	86.2	223	7	ADH88125
90	25	86.2	224	3	AAV84826
91	25	86.2	233	7	ABO60849
92	25	86.2	238	8	ADY13154
93	25	86.2	239	6	ADA34579
94	25	86.2	259	4	AAU64295
95	25	86.2	259	6	ABM60814
96	25	86.2	266	8	ADJ49926
97	25	86.2	266	8	ADJ49926

Adn25218	Bacterial
Abg78151	Human Fv
Abg92021	Antibody
Abg91842	Human ant
Aau42688	Propionib
Abm39207	Propionib
Aae14569	Human rho
Ada13449	Human rho
Ada13415	Human rho
Adg47134	Human rho
Adg47100	Human rho
Ada13459	Mouse rho
Adg47144	Mouse rho
AAO90242	C glutami
ABO75198	Pseudomon
Aau44808	Propionib
Abm41327	Propionib
Aeb54740	Fusarium
Aam2945	Human imm
Aau56719	Propionib
ABM53238	Propionib
ABP73581	Candida a
Agg98915	E. coli g
Abu15252	Protein e
ADJ45133	Bacterial
ADY13333	Plant ful
ABU28269	Protein e
ADX92867	Plant ful
Aay35225	Chlamydia
ADC87283	Human GPC
ABO62389	Klebsiell
ADX91171	Plant ful
ADY04822	Plant ful
ABE66060	Drosophil
ADK01781	Hepatitis
ADN48220	Thermococ
ADZ67861	Modified
ADZ67863	Modified
ADZ67864	Modified
ADZ67862	Modified
Aay12754	Human 5'
ADS06874	Staphyloc
ADS07022	Staphyloc
ADS04516	Staphyloc
ADI60240	Secreted
ABP08294	Human ORF
AGG18780	Zea may
AAW90282	Human imm
AAO28861	Zea may
ABM65637	Propionib
ABP32292	Human ORF
ABO79679	Pseudomon
ADC97061	E. faeciu
AAV11311	S. pneumo
AAU45601	Propionib
AAU42587	Propionib
ABM39106	Propionib
ADT57210	Plant pol
AAU56128	Propionib
ABM52647	Propionib
ABM93814	M. xanthu
AAV84827	A. snooze
ABO61727	Klebsiell
ADT87198	Yeast Str
ADH88125	Enterococ
AAV84826	A. snooze
ABO60849	Klebsiell
ADY13154	Plant ful
ADA34579	Acinetoba
Aau64295	Propionib
ABM60814	Propionib
ADJ49926	Oil-assoc

KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

OS Homo sapiens.

XX WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in

PT physiological phenomena such as cell rolling, metastasis and

PT inflammation, for treating autoimmune, inflammatory or cardiovascular

PT diseases, and cancer.

XX PS Claim 1; Page 228; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 4

AD128369

ID AD128369 standard; peptide; 6 AA.

XX AC AD128369;

XX DT 06-MAY-2004 (first entry)

XX DE Human CDR3 peptide, used in therapeutic composition.

XX KW Human; antibody; scFv; complementarity determining region; drug delivery;

XX KW cancer; therapy.

XX OS Homo sapiens.

XX PN WO2004002528-A1.

XX PD 08-JAN-2004.

XX PF 30-JUN-2003; 2003WO-US020604.

XX PR 01-JUL-2002; 2002US-00189025.

XX PA (SAVI-) SAVIENT PHARM INC.

XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;

XX DR WPI; 2004-099189/10.

XX Composition comprising an agent and/or antibody or its fragment, useful
PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.

XX PS Claim 14; SEQ ID NO 4; 58pp; English.

XX The present sequence is that of a human antibody complementarity
CC determining region 3 (CDR3). The invention relates to compositions
CC utilising an agent and an antibody or its fragment. The agent is a toxin,
CC radioisotope or pharmaceutical agent such as doxorubicin. It is complexed
CC or combined with or conjugated to the antibody or its fragment. The
CC antibody may have a first hypervariable region comprising the present
CC sequence. The agent and/or antibody can be present in the composition is
CC a sub-clinical amount, i.e. less than the amount generally found to be
CC clinically effective when the agent is administered alone. The
CC composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumour cells or leukaemia cells, an increase in number of
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
CC susceptibility of disease cells to damage by anti-disease agents, and the
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

Db 1 MRAPVI 6

RESULT 5

ADJ57364

ID ADJ57364 standard; peptide; 6 AA.

XX AC ADJ57364;

XX DT 06-MAY-2004 (first entry)

XX DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32 CDR3.

XX KW P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;

XX KW antiinflammatory; immunosuppressive; complementarity determining region;

XX KW human.

XX OS Homo sapiens.

XX PN WO2004003166-A2.

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PD 08-JAN-2004.
XX OS Homo sapiens.
XX US2004202665-A1.
XX PN
XX 14-OCT-2004.
XX PD
XX 30-JUN-2003; 2003US-00610843.
XX PF
XX 01-JUL-2002; 2002US-0393453P.
XX PR
XX (SAVI-) SAVIENT PHARM INC.
XX PA
XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
XX PI Hoch Mar- Chaim H;
XX PR
XX WPI; 2004-203378/19.
XX DR
XX Novel antibody or its fragment that binds to an epitope of P-Selectin-
XX PT Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
XX PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
XX PT patient.
XX PS Claim 2; SEQ ID NO 2; 106pp; English.
XX CC
XX The present sequence is that of the heavy chain complementarity
XX CC determining region 3 (CDR3) of L32 ABJ57363, an scFv antibody fragment
XX CC that binds P-selectin glycoprotein ligand-1 (PSGL-1). L32 was identified
XX CC by screening a phage library, which had diversity only in the heavy chain
XX CC CDR3 regions, against a leukaemia cell to select specific antibodies that
XX CC recognised leukaemia cell surface determinants, wherein the specific
XX CC receptor was not previously known or characterised. The invention relates
XX CC to an antibody or its fragment having the binding capabilities of L32 and
XX CC comprising at least one of the heavy chain CDRs of L32. Such antibodies
XX CC can be used in therapeutic, diagnostic, prognostic and staging methods.
XX CC Pharmaceutical compositions comprising such antibodies are used to treat
XX CC conditions related to: inhibiting or treating cell rolling, inflammation,
XX CC autoimmune disease, infection (e.g. HIV infection), metastasis, and
XX CC growth and/or replication of tumour cells; increasing the mortality of
XX CC tumour cells; inhibiting growth and/or replication of leukaemia cells;
XX CC inhibiting growth and/or replication of leukaemia cells; increasing the
XX CC mortality rate of leukaemia cells; altering the susceptibility of
XX CC diseased cells to damage by anti-disease agents; increasing the
XX CC susceptibility of tumour cells to damage by anti-cancer agents;
XX CC increasing the susceptibility of leukaemia cells to damage by anti-
XX CC leukaemia agents; inhibiting increase in number of tumour cells in a
XX CC patient; decreasing the number of tumour cells in a patient; inhibiting
XX CC increase in number of leukaemia cells in a patient; and decreasing the
XX CC number of leukaemia cells in a patient. Other methods are provided to
XX CC induce antibody-dependent cell-mediated cytotoxicity or stimulate natural
XX CC killer or T cells using the antibodies. A method of purging tumour cells
XX CC from a patient involves incubating the cells with the antibody.
XX SQ
XX Sequence 6 AA;
XX Query Match 100.0%; Score 29; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MRAPVI 6
XX Db 1 MRAPVI 6
XX RESULT 6
XX ADS82029
XX ID ADS82029 standard; peptide; 6 AA.
XX AC
XX ADS82029;
XX 30-DEC-2004 (first entry)
XX DT
XX Human scFv antibody CDR3 hypervariable region.
XX DE
XX cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
XX KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
XX KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
XX KW vasotropic; immunosuppressive; cardiovascular-gen; ophthalmological.
XX
XX 08-JAN-2004.
XX OS Homo sapiens.
XX XX US2004202665-A1.
XX PN
XX 14-OCT-2004.
XX PD
XX 30-JUN-2003; 2003US-00610843.
XX PF
XX 01-JUL-2002; 2002US-0393453P.
XX PR
XX (LAZA/) LAZAROVITS J.
XX PA (NIMR/) NIMROD A.
XX PA (HOCH/) HOCH M H.
XX PA (LEVA/) LEVANON A.
XX XX
XX Lazarovits J, Nimrod A, Hoch MH, Levanon A;
XX XX WPI; 2004-746943/73.
XX DR
XX Composition useful for treating diseases e.g., inflammatory diseases,
XX PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
XX PT retinopathic diseases, comprises agent and antibody or its fragment.
XX XX
XX Disclosure; SEQ ID NO 4; 22pp; English.
XX PS
XX The invention relates to a composition which comprises an agent and an
XX CC antibody or its fragment. The composition is useful for inhibiting cell
XX CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
XX CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
XX CC and/or cell-platelet complex formation, aggregation or adhesion, increase
XX CC in number of tumour cells or growth and/or replication of tumour or
XX CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
XX CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
XX CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
XX CC ameliorating the effect of a disease, preventing a disease, treating a
XX CC disease, or inhibiting the progress of a disease. The composition is
XX CC useful for therapeutic treatment, where antibody or its fragment and the
XX CC agent are administered separately. The antibody or its fragment is
XX CC administered prior to or subsequent to the agent. The composition is
XX CC useful for treating diseases such as inflammatory diseases, diseases
XX CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
XX CC diseases involving abnormal or pathogenic aggregation, autoimmune
XX CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
XX CC by sulphated tyrosine-dependent protein-protein interactions or diseased
XX CC cells. The present sequence represents the human scFv antibody CDR3
XX CC hypervariable region.
XX SQ
XX Sequence 6 AA;
XX Query Match 100.0%; Score 29; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MRAPVI 6
XX Db 1 MRAPVI 6
XX RESULT 7
XX ADT63079
XX ID ADT63079 standard; peptide; 6 AA.
XX XX
XX AC ADT63079;
XX 13-JAN-2005 (first entry)
XX DT
XX Human hypervariable region CDR3.
XX DE
XX P-selectin Glycoprotein Ligand-1; PSGL-1; heavy chain;
XX KW complementarity determining region; CDR3;
XX KW T cell-acute lymphoblastic leukaemia cell;
XX KW acute myelogenous leukaemia cell; B-leukaemia cell;

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KW B cell-chronic lymphocytic leukaemia; multiple myeloma cell;
KW inflammation; HIV infection; auto-immune disease; metastasis;
KW tumour cell; anti-cancer; cytostatic; antimicrobial; antiinflammatory;
KW immunosuppressive; anti-HIV; human; scfv antibody fragment;
KW hypervariable region.
OS Homo sapiens.
XX US20040208877-A1.
XX 21-OCT-2004.
XX 30-JUN-2003; 2003US-00611588.
XX 01-JUL-2002; 2002US-0393491P.
XX (LEVA/) LEVANON A.
XX (BENL/) BEN-LEVY R.
XX (PLAK/) PLAKSIN D.
XX (SZAN/) SZANTON E.
XX (HAGA/) HAGAI Y.
XX (MARC/) MAR-CHAIM H H.
XX Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
PI Mar-Chaim H;
XX WPI; 2004-765453/75.
XX New antibody or its fragment that binds to an epitope of P-selectin
PT Glycoprotein Ligand-1 (PSGL-1), useful for manufacturing a medicament for
PT treating e.g., inflammation, HIV infection, auto-immune disease, and
PT metastasis.
XX Claim 2; SEQ ID NO 2; 49pp; English.
XX The present invention relates to an antibody or its fragment that binds
XX to an epitope of P-selectin Glycoprotein Ligand-1 (PSGL-1) comprising a
XX sequence comprising 280 amino acids (SEQ ID NO: 1) fully defined in the
XX specification, that has the binding capabilities of an scfv of SEQ ID NO:
XX 1, or comprising one heavy chain complementarity determining region
XX (CDR). The heavy chain CDR comprises the sequences given in the
XX specification as SEQ ID NO: 2, 3, or 4. Two or three heavy chain CDRs are
XX selected from SEQ ID NO: 2, 3, and 4. The antibody or its fragment
XX comprises at least one framework variable region from germline DP32. It
XX may be a substantially circular or looped peptide or polypeptide. The
XX epitope comprises at least one sulphated moiety. The antibody or its
XX fragment may bind or cross-react with two or more epitopes, each epitope
XX comprising one or more sulphated tyrosine residues, preferably comprising
XX at least one cluster of two or more acidic amino acids. It may bind to an
XX epitope on at least one cell selected from T cell-acute lymphoblastic
XX leukaemia cells, acute myelogenous leukaemia cells, B-leukaemia cells, B
XX cell-chronic lymphocytic leukaemia, and multiple myeloma cells. It may
XX bind to an epitope on a lipid, carbohydrate, peptide glycolipid,
XX glycoprotein, lipoprotein, and/or lipopolyaccharide molecule. It may be
XX coupled to or complexed with an agent selected from anti-cancer, anti-
XX leukaemic, anti-metastasis, anti-neoplastic, anti-disease, anti-adhesion,
XX anti-thrombosis, anti-restenosis, anti-autoimmune, anti-aggregation, anti-
XX bacterial, anti-viral, and anti-inflammatory agents, preferably anti-
XX viral agent selected from acyclovir, ganciclovir and zidovudine. The
XX agent may be selected from toxins, radioisotopes, imaging agents, and
XX pharmaceutical agents. The antibody or its fragment may be coupled to or
XX complexed with a vehicle or carrier that can be coupled or complexed to
XX more than one agent. The vehicle or carrier is selected from dextran,
XX lipophilic polymers, HPMA, and liposomes, and their derivatives and
XX modifications. A pharmaceutical composition comprising the antibody or
XX its fragments is useful in a method for treating a disease or cell
XX rolling in a patient, for ameliorating the effects of inflammation,
XX preventing inflammation, for treating an infection, i.e. caused by HIV,
XX where the administration prevents cell entry of HIV, for treating an auto
XX -immune disease, for treating metastasis, or for treating growth and/or
XX replication of tumour or leukaemia cells. The pharmaceutical composition
XX is also useful for manufacturing a medicament for treating the diseases.

CC The pharmaceutical composition is useful for increasing the mortality
CC rate of tumour or leukaemia cells, altering the susceptibility of
CC diseased, tumour or leukaemia cells to damage by anti-disease agents or
CC anti-cancer agents, inhibiting increase in number or decreasing number of
CC tumour or leukaemia cells in a patient having a tumour or leukaemia,
CC eliciting antibody dependent cell-mediated cytotoxicity or stimulating a
CC natural killer cell or a T cell, diagnosing, prognosing or staging
CC metastasis, tumour cell, or leukaemia in a patient, or for purging tumour
CC cells from a patient. The present sequence represents a human
CC hypervariable region (CDR) that may be used in the antibody of the
CC invention.
XX
XX SQ Sequence 6 AA;
XX Query Match 100.0%; Score 29; DB 8; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db |||||
1 MRAPVI 6
RESULT 8
ADX01129
ID ADX01129 standard; peptide; 6 AA.
XX
XX AC ADX01129;
XX 21-APR-2005 (first entry)
XX CDR3 not included in consensus sequence for cancer cell binding antibody.
XX DE
XX KW antibody; cancer; diagnosis; tumor; HIV infection; autoimmune disease;
XX metastasis; leukemia; platelet; antiaggregant; restenosis;
XX antibody dependent cell-mediated cytotoxicity; apoptosis;
XX natural killer cell; T-lymphocyte; inflammation; cardiovascular disease;
XX retinopathy; anti-HIV; cytostatic; immunosuppressive; antiinflammatory;
XX cardiovascular-gen.; ophthalmological;
XX complementarity determining region 3; CDR3.
XX Unidentified.
XX OS
XX PN WC2005010153-A2.
XX XX
XX PD 03-FEB-2005.
XX PF 30-JUN-2004; 2004WO-US021002.
XX PR 30-JUN-2003; 2003US-00611238.
XX PA (SAVI-) SAVIENT PHARM INC.
XX PI Plaksin D, Levanon A, Szanton E, Hagai Y, Ben-Levy R, Nisgav Y;
XX PI Szrajber T, Kanfi Y;
XX DR WPI; 2005-132536/14.
XX Novel antibody e.g., S15 antibody or their fragments useful for purging
XX tumor cells from patient or for treating autoimmune diseases,
XX inflammatory diseases, cardiovascular diseases or retinopathic diseases.
XX PS Disclosure; SEQ ID NO 4; 134pp; English.
XX The invention relates to antibodies e.g. S15 antibody, or their fragments
XX that bind to cancer cells. The antibodies or their fragments comprise a
XX consensus sequence (given as SEQ ID No:3 in the specification) of X1-X2-
XX X3-Pro-X5-X6, where X1 and X6 are hydrophobic amino acids and X2, X3 and
XX X5 are any amino acid. Also described are (i) a composition comprising
XX the antibody and a carrier, (ii) a diagnostic, prognostic or staging kit
XX comprising the antibody and an imaging agent, (iii) an isolated or
XX purified DNA sequence encoding the antibody, (iv) an expression vector
XX comprising the DNA sequence, (v) a recombinant host cell comprising the

expression vector, (vi) a method of producing the antibody, (vii) a polypeptide comprising the consensus sequence, (viii) a method of selecting an antibody or their fragments or a polypeptide, (ix) an antibody or their fragment produced by the method, (x) a library of immunoglobulin binding domains, (xi) a small inorganic molecule that binds to a sulfated epitope of PSGL-1, GP1b and/or CCR5, and (xii) a composition comprising a small inorganic molecule. The antibody of the invention is useful for diagnosing, prognosing, or staging a disease in a patient which involves providing a sample containing a cell from the patient and determining whether the antibody binds to the cell of the patient, thus indicating that the patient is at risk or has the disease. The antibody is useful for purging tumor cells from a patient which involves providing a sample containing cells from the patient, and incubating the cells from the patient with the antibody, where purging occurs under ex vivo conditions. A composition comprising the antibody is useful for treating a disease (e.g. infection caused by HIV) or cell rolling, inhibiting autoimmune disease, metastasis or growth and/or replication of tumor or leukemic cells e.g. B-CLL cells, increasing the mortality rate of tumor or leukemic cells, altering the susceptibility of disease cells to damage by anti-disease agents, increasing the susceptibility of tumor or leukemic cells to damage by anticancer or antileukemic agents, inhibiting platelet aggregation or restenosis eliciting antibody dependent cell-mediated cytotoxicity (ADCC), eliciting apoptosis in leukemic cells, or stimulating a natural killer (NK) cell or a T cell. ADCC is mediated by effector cells e.g. natural killer or monocyte cells. The composition is also useful for producing medicament for treating a disease. The library of immunoglobulin binding domains is useful for selecting a sulfated epitope that binds to the antigen-binding domain. The antibody is useful for treating cancer, leukemia, autoimmune diseases, inflammatory diseases, HIV infection, cardiovascular diseases, and retinopathic diseases. This sequence represents a complementarity determining region 3 (CDR3) that is not included in the consensus sequence for the antibody of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 1 MRAPVI 6

RESULT 9

ID ADY78323 standard; peptide; 6 AA.

AC ADY78323;

DT 16-JUN-2005 (first entry)

XX Single chain Fv antibody CDR3 region peptide SEQ ID NO:4.

XX antibody; metastasis; cancer; autoimmune disease; cytostatic; anti-HIV;
KW antinflammatory; immunosuppressive; vasotropic; cardiovascular-gen.;
KW cardiant; infection; inflammation; leukemia; Fv.

XX Synthetic.

XX US2005069955-A1.

XX 31-MAR-2005.

XX 30-JUN-2004; 2004US-00880922.

XX 30-JUN-2003; 2003US-0484061P.

XX (PLAK/) PLAKSIN D.

XX (LEVA/) LEVANON A.

XX (SZAN/) SZANTON E.

XX (HAGA/) HAGAY Y.

PA

(BENL/) BEN-LEVY R.

PA (NISG/) NISGAV Y.

XX (KANF/) KANFI Y.

PI Plaksin D, Levanon A, Szanton E, Hagay Y, Ben-Levy R, Nisgav Y;

XX Kanfi Y;

DR WPI; 2005-261644/27.

XX Novel antibody or its fragment comprising consensus sequence that binds to cancer cell, useful for diagnosing or treating diseases such as cancer, autoimmune diseases and inflammatory diseases.

XX Example 1; SEQ ID NO 4; 74pp; English.

XX The invention relates to an antibody or its fragment (I) comprising the consensus sequence X1-X2-X3-Pro-X5-X6, where X1 and X6 are hydrophobic amino acids and X2, X3 and X5 are any amino acid. Also described: (1) a pharmaceutical composition (II), comprising (I) and a carrier; (2) a diagnostic, prognostic, or staging kit (K1), comprising (I) and an imaging agent; (3) an isolated or purified DNA sequence (III) encoding (I); (4) an expression vector (IV) comprising (III); (5) a recombinant host cell (V) comprising (IV); (6) producing (I); (7) a library (VII) of immunoglobulin binding domains, comprising a diverse antigen binding domain for complementary binding, where (VII) has diversity only in heavy chain CDR3; (8) a small inorganic molecule (VIII) capable of binding to a sulfated epitope of PSGL-1, GP1b, and/or CCR5; and (9) a pharmaceutical composition (IX), comprising (VIII). (II) is useful for treating a disease, cell rolling, an infection (where the infection is caused by HIV and the administration of (II) prevents entry of HIV), and inflammation. (II) can also be used for inhibiting autoimmune disease, inhibiting metastasis, inhibiting growth and/or replication of tumor cells, increasing the mortality rate of tumor cells, inhibiting growth and/or replication of leukemia cells, increasing the mortality rate of leukemia cells, inhibiting growth and/or replication of B-CLL cells, altering the susceptibility of diseased cells to damage by anti-cancer agents, increasing the susceptibility of leukemia cells to damage by anti-leukemia agents, increasing the susceptibility of B-CLL cells to damage by anti-leukemia agents, inhibiting platelet aggregation, inhibiting restenosis, eliciting antibody dependent cell-mediated cytotoxicity (ADCC) (mediated by effector cells comprising of natural killer (NK) or monocytic cells), eliciting apoptosis in leukemia cells, stimulating a NK cell or a T cell, and manufacturing medicament for treating a disease. (I) is useful for diagnosing, prognosing or staging a disease in a patient, which involves providing a sample containing a cell from the patient and determining whether (I) binds to the cell of the patient, and so indicates that the patient is at risk for or has the disease. (I) is useful for purging tumor cells from a patient, which involves providing a sample containing cells from the patient and incubating the cells from the patient with (I), where the purging occurs ex vivo. (VII) is useful for selecting a sulfated epitope, which involves providing (VII), panning (VII) for a sulfated epitope that binds to the antigen binding domain, and isolating the sulfated epitope. (V) is useful for producing (I). (II) is useful for treating cardiovascular diseases such as myocardial infarction and inflammatory diseases. The present sequence represents a scFv antibody CDR3 region peptide, which is given in the exemplification of the present invention.

SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

DB 1 MRAPVI 6

RESULT 10

ABG78329

ID ABG78329 standard; protein; 246 AA.

XX

AC ABG78329;
 XX 15-NOV-2002 (first entry)
 XX Human Fv molecule hypervariable region related peptide #204.
 DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; deFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.
 OS WO200259264-A2.
 XX 01-AUG-2002.
 XX 31-DEC-2001; 2001WO-US049440.
 XX 29-DEC-2000; 2000US-00751181.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI; 2002-619166/66.
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX Disclosure; Page 44-45; 232pp; English.
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX SQ Sequence 246 AA;
 Query Match 100.0%; Score 29; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRAPVI 6
 Db 100 MRAPVI 105
 RESULT 11
 ID ABG92026 standard; protein; 246 AA.
 XX AC ABG92026;
 XX 04-DEC-2002 (first entry)
 DT Antibody protein #5.
 DE Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 XX metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW

KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 XX sulphated tyrosine-dependent protein-protein interaction.
 OS Unidentified.
 XX WO200253700-A2.
 XX 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 XX 29-DEC-2000; 2000US-00751181.
 XX 29-DEC-2000; 2000US-0258948P.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI; 2002-674776/72.
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX Disclosure; Fig 52; Opp; English.
 XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents an antibody protein of the
 CC invention
 XX SQ Sequence 246 AA;
 Query Match 100.0%; Score 29; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRAPVI 6
 Db 100 MRAPVI 105
 RESULT 12
 ID ABG78334 standard; protein; 256 AA.
 XX AC ABG78334;
 XX 15-NOV-2002 (first entry)
 DT Human Fv molecule hypervariable region related peptide #209.
 DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 XX

PN WO200253700-A2.
 XX 11-JUL-2002.
 PD 31-DEC-2001; 2001WO-US049442.
 PF 29-DEC-2000; 2000US-00751181.
 PP 29-DEC-2000; 2000US-0258948P.
 PR (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 XX Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 PI WPI; 2002-674776/72.
 XX Novel isolated epitope present on cancer cells and important in
 XX physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX Disclosure; Page 309-310; Opp: English.
 XX The invention relates to an isolated epitope present on cancer cells and
 XX important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 XX SQ Sequence 266 AA;
 Query Match 100.0%; Score 29; DB 5; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 MRAPVI 6
 Db 121 MRAPVI 126
 RESULT 15
 ABG78150
 ID ABG78150 standard; protein; 277 AA.
 XX
 XX AC ABG78150;
 XX 15-NOV-2002 (first entry)
 DT Human Fv molecule hypervariable region related peptide #25.
 XX
 XX DE
 XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX
 XX OS Homo sapiens.
 XX PN WO200259264-A2.

XX 01-AUG-2002.
 XX 31-DEC-2001; 2001WO-US049440.
 XX 29-DEC-2000; 2000US-00751181.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI; 2002-619166/66.
 XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.
 XX Claim 4; Page 155-156; 232pp; English.
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX
 XX SQ Sequence 277 AA;
 Query Match 100.0%; Score 29; DB 5; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 MRAPVI 6
 Db 121 MRAPVI 126
 RESULT 16
 ABG91841
 ID ABG91841 standard; protein; 277 AA.
 XX
 XX AC ABG91841;
 XX 04-DEC-2002 (first entry)
 DT Human antibody fragment #25.
 XX
 XX DE
 XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX
 XX OS Homo sapiens.
 XX PN WO200253700-A2.
 XX 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 XX 29-DEC-2000; 2000US-00751181.

29-DEC-2000; 2000US-0258948P.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richer T, Amit B, Kooperman L, Peretz T, Levanon A;
WPI; 2002-674776/72.
Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.
Claim 23; Page 233-234; Opp; English.
The invention relates to an isolated epitope present on cancer cells and
important in physiological phenomena such as cell rolling, metastasis and
inflammation, where the epitope is capable of being bound by an antibody,
its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents a human antibody fragment
of the invention
SQ Sequence 277 AA;
Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRAPVI 6
Db 121 MRAPVI 126
RESULT 17
ADI28366
ID ADI28366 standard; protein; 277 AA.
XX AC ADI28366;
XX 06-MAY-2004 (first entry)
XX DT
XX DE Human scFv fragment Y1, binds to platelets.
XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX (SAVI-) SAVIENT PHARM INC.
XX PA

29-DEC-2000; 2000US-0258948P.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richer T, Amit B, Kooperman L, Peretz T, Levanon A;
WPI; 2002-674776/72.
Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.
Claim 23; Page 233-234; Opp; English.
The invention relates to an isolated epitope present on cancer cells and
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inflammation, where the epitope is capable of being bound by an antibody,
its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents a human antibody fragment
of the invention
SQ Sequence 277 AA;
Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRAPVI 6
Db 121 MRAPVI 126
RESULT 17
ADI28366
ID ADI28366 standard; protein; 277 AA.
XX AC ADI28366;
XX 06-MAY-2004 (first entry)
XX DT
XX DE Human scFv fragment Y1, binds to platelets.
XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX (SAVI-) SAVIENT PHARM INC.
XX PA

29-DEC-2000; 2000US-0258948P.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richer T, Amit B, Kooperman L, Peretz T, Levanon A;
WPI; 2002-674776/72.
Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.
Claim 23; Page 233-234; Opp; English.
The invention relates to an isolated epitope present on cancer cells and
important in physiological phenomena such as cell rolling, metastasis and
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its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents a human antibody fragment
of the invention
SQ Sequence 277 AA;
Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRAPVI 6
Db 121 MRAPVI 126
RESULT 17
ADI28366
ID ADI28366 standard; protein; 277 AA.
XX AC ADI28366;
XX 06-MAY-2004 (first entry)
XX DT
XX DE Human scFv fragment Y1, binds to platelets.
XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX (SAVI-) SAVIENT PHARM INC.
XX PA

29-DEC-2000; 2000US-0258948P.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richer T, Amit B, Kooperman L, Peretz T, Levanon A;
WPI; 2002-674776/72.
Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.
Claim 23; Page 233-234; Opp; English.
The invention relates to an isolated epitope present on cancer cells and
important in physiological phenomena such as cell rolling, metastasis and
inflammation, where the epitope is capable of being bound by an antibody,
its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents a human antibody fragment
of the invention
SQ Sequence 277 AA;
Query Match 100.0%; Score 29; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRAPVI 6
Db 121 MRAPVI 126
RESULT 17
ADI28366
ID ADI28366 standard; protein; 277 AA.
XX AC ADI28366;
XX 06-MAY-2004 (first entry)
XX DT
XX DE Human scFv fragment Y1, binds to platelets.
XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX (SAVI-) SAVIENT PHARM INC.
XX PA

29-DEC-2000; 2000US-0258948P.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richer T, Amit B, Kooperman L, Peretz T, Levanon A;
WPI; 2002-674776/72.
Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.
Claim 23; Page 233-234; Opp; English.
The invention relates to an isolated epitope present on cancer cells and
important in physiological phenomena such as cell rolling, metastasis and
inflammation, where the epitope is capable of being bound by an antibody,
its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents a human antibody fragment
of the invention
SQ Sequence 277 AA;
Query Match 100.0%; Score 29

XX WPI; 2004-746943/73.
 XX Composition useful for treating diseases e.g., inflammatory diseases,
 PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
 XX retinopathic diseases, comprises agent and antibody or its fragment.
 PS Claim 13; SEQ ID NO 2; 22pp; English.
 XX The invention relates to a composition which comprises an agent and an
 CC antibody or its fragment. The composition is useful for inhibiting cell
 CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
 CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
 CC and/or cell-platelet complex formation, aggregation or adhesion, increase
 CC in number of tumour cells or growth and/or replication of tumour or
 CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
 CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
 CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
 CC ameliorating the effect of a disease, preventing a disease, treating a
 CC disease, or inhibiting the progress of a disease. The composition is
 CC useful for therapeutic treatment, where antibody or its fragment and the
 CC agent are administered separately. The antibody or its fragment is
 CC administered prior to or subsequent to the agent. The composition is
 CC useful for treating diseases such as inflammatory diseases, diseases
 CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
 CC diseases involving abnormal or pathogenic aggregation, autoimmune
 CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
 CC by sulphated tyrosine-dependent protein-protein interactions or diseased
 CC cells. The present sequence represents the human platelet binding scfv
 XX antibody fragment Y17.
 SQ Sequence 278 AA;

Query Match 100.0%; Score 29; DB 8; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 122 MRAPVI 127
 RESULT 21
 ADI28368
 ID ADI28368 standard; protein; 280 AA.
 XX
 AC ADI28368;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human scFv fragment L32, binds to leukaemia cells.
 XX
 KW Human; antibody; scFv; leukaemia; drug delivery; cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004002528-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020604.
 XX
 PR 01-JUL-2002; 2002US-00189025.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
 XX
 DR WPI; 2004-099189/10.
 XX
 XX Composition comprising an agent and/or antibody or its fragment, useful
 PT for treating autoimmune disease, thrombosis, restenosis, metastasis, or
 PT for inhibiting growth and/or replication of tumor cells or leukemia
 . PT

PT cells.

XX Claim 13; SEQ ID NO 3; 58pp; English.

XX The present sequence is the protein sequence of human scFv fragment L32.
 CC This antibody was identified by screening a human antibody phage library
 CC that has diversity only in the heavy chain CDR3 regions. Leukaemia cells
 CC were screened to select specific antibodies that recognise leukaemia cell
 CC surface determinants. The invention relates to compositions utilising an
 CC agent and an antibody or its fragment. The agent is a toxin, radioisotope
 CC or pharmaceutical agent such as doxorubicin. It is complexed or combined
 CC with or conjugated to the antibody or its fragment. The agent and/or
 CC antibody can be present in the composition is a sub-clinical amount, i.e.
 CC less than the amount generally found to be clinically effective when the
 CC agent is administered alone. The composition is used in claimed methods
 CC of: inhibiting cell rolling, inflammation, thrombosis, restenosis,
 CC metastasis, the growth and/or replication of tumour cells or leukaemia
 CC cells, an increase in number of tumour or leukaemia cells, cell-cell,
 CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
 CC complex formation, aggregation or adhesion; increasing the mortality rate
 CC of tumour or leukaemia cells, the susceptibility of disease cells to
 CC damage by anti-disease agents, and the susceptibility of tumour or
 CC leukaemia cells to damage by anti-cancer agents; and ameliorating the
 CC effects of a disease, preventing a disease, treating a disease or
 CC inhibiting the progress of a disease.
 XX

SQ Sequence 280 AA;

Query Match 100.0%; Score 29; DB 8; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 124 MRAPVI 129

RESULT 22
 ADJ57363
 ID ADJ57363 standard; protein; 280 AA.
 XX
 AC ADJ57363;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE P-selectin glycoprotein ligand-1-binding scFv antibody fragment L32.
 XX
 KW P-selectin glycoprotein ligand-1; PSGL-1; antibody; scFv; cytostatic;
 KW antiinflammatory; immunosuppressive; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 53..60
 FT /label= CDR1
 FT /note= "Specifically referred to in Claim 2"
 FT Region 75..90
 FT /label= CDR2
 FT /note= "Specifically referred to in Claim 2"
 FT Region 124..129
 FT /label= CDR3
 FT /note= "Specifically referred to in Claim 2"
 XX
 PN WO2004003166-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020602.
 XX
 PR 01-JUL-2002; 2002US-00189032.
 XX
 PA (SAVI-) SAVIENT PHARM INC.
 XX
 XX

PI Levanon A, Ben-Levy R, Plaksin D, Szanton E, Hagai Y;
 PI Hoch Mar- Chaim H;
 XX WPI; 2004-203378/19.
 DR
 XX Novel antibody or its fragment that binds to an epitope of P-Selectin-
 PT Glycoprotein Ligand-1, useful for diagnosing/prognosing inflammation,
 PT infection, auto-immune disease, metastasis, tumor/leukemia cell in
 PT patient.
 XX
 PS Claim 1; SEQ ID NO 1; 106pp; English.
 XX
 CC The present sequence is that of an scFv antibody fragment, designated
 CC L32, that binds P-selectin glycoprotein ligand-1 (PSGL-1). The antibody
 CC was identified by screening a phage library, which had diversity only in
 CC the heavy chain CDR3 regions, against a leukemia cell to select specific
 CC antibodies that recognised leukemia cell surface determinants, wherein
 CC the specific receptor was not previously known or characterised. The
 CC invention relates to an antibody or its fragment having the binding
 CC capabilities of L32. Such antibodies can be used in therapeutic,
 CC diagnostic, prognostic and staging methods. Pharmaceutical compositions
 CC comprising such antibodies are used to treat conditions related to:
 CC inhibiting or treating cell rolling, inflammation, autoimmune disease,
 CC infection (e.g. HIV infection), metastasis, and growth and/or replication
 CC of tumour cells; increasing the mortality of tumour cells; inhibiting
 CC growth and/or replication of tumour cells; inhibiting growth and/or
 CC replication of leukemia cells; increasing the mortality rate of
 CC leukemia cells; altering the susceptibility of diseased cells to damage
 CC by anti-disease agents; increasing the susceptibility of tumour cells to
 CC damage by anti-cancer agents; increasing the susceptibility of leukemia
 CC cells to damage by anti-leukemia agents; inhibiting increase in number
 CC of tumour cells in a patient; decreasing the number of tumour cells in a
 CC patient; inhibiting increase in number of leukemia cells in a patient;
 CC and decreasing the number of leukemic cells in a patient. Other methods
 CC are provided to induce antibody-dependent cell-mediated cytotoxicity or
 CC stimulate natural killer or T cells using the antibodies. A method of
 CC purging tumour cells from a patient involves incubating the cells with
 CC the antibody.
 XX
 SQ Sequence 280 AA;
 Query Match 100.0%; Score 29; DB 8; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 Db 124 MRAPVI 129
 RESULT 23
 ADS82028
 ID ADS82028 standard; protein; 280 AA.
 XX
 AC ADS82028;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE Human leukaemia cell binding scFv antibody fragment L32.
 XX
 KW cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
 KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
 KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
 KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.
 XX
 OS Homo sapiens.
 XX
 PN US2004202665-A1.
 XX
 PD 14-OCT-2004.
 XX
 PF 30-JUN-2003; 2003US-00610843.
 XX

PR 01-JUL-2002; 2002US-0393453P.
 XX
 PA (LAZA/) LAZAROVITS J.
 PA (NIMR/) NIMROD A.
 PA (HOCH/) HOCH M H.
 PA (LEVA/) LEVANON A.
 XX
 PI Lazarovits J, Nimrod A, Hoch MH, Levanon A;
 XX
 DR WPI; 2004-746943/73.
 XX
 CC Composition useful for treating diseases e.g., inflammatory diseases, or
 CC thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
 CC retinopathic diseases, comprises agent and antibody or its fragment.
 PT
 XX
 PS Claim 13; SEQ ID NO 3; 22pp; English.
 XX
 CC The invention relates to a composition which comprises an agent and an
 CC antibody or its fragment. The composition is useful for inhibiting cell
 CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
 CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
 CC and/or cell-platelet complex formation, aggregation or adhesion, increase
 CC in number of tumour cells or growth and/or replication of tumour or
 CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
 CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
 CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
 CC ameliorating the effect of a disease, preventing a disease, treating a
 CC disease, or inhibiting the progress of a disease. The composition is
 CC useful for therapeutic treatment, where antibody or its fragment and the
 CC agent are administered separately. The antibody or its fragment is
 CC administered prior to or subsequent to the agent. The composition is
 CC useful for treating diseases such as inflammatory diseases, diseases
 CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
 CC diseases involving abnormal or pathogenic aggregation, autoimmune
 CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
 CC by sulphated tyrosine-dependent protein-protein interactions or diseased
 CC cells. The present sequence represents the human leukaemia cell binding
 CC scFv antibody fragment L32.
 XX
 SQ Sequence 280 AA;
 Query Match 100.0%; Score 29; DB 8; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 Db 124 MRAPVI 129
 RESULT 24
 ADT63078
 ID ADT63078 standard; protein; 280 AA.
 XX
 AC ADT63078;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human scFv antibody fragment binding PSGL-1.
 XX
 KW P-selectin Glycoprotein Ligand-1; PSGL-1; heavy chain;
 KW complementarity determining region; CDR;
 KW T cell-acute lymphoblastic leukaemia cell;
 KW acute myelogenous leukaemia cell; B-leukaemia cell;
 KW B cell-chronic lymphocytic leukaemia; multiple myeloma cell;
 KW inflammation; HIV infection; auto-immune disease; metastasis;
 KW tumour cell; anti-cancer; cytostatic; antimicrobial; antiinflammatory;
 KW immunosuppressive; anti-HIV; human; scFv antibody fragment.
 XX
 OS Homo sapiens.
 XX
 PN US2004208877-A1.
 XX

CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactanmannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 442 AA;
 Query Match 100.0%; Score 29; DB 8; Length 442;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 77 MRAPVI 82

RESULT 26
 ABG78151
 ID ABG78151 standard; protein; 464 AA.
 AC ABG78151;
 XX 15-NOV-2002 (first entry)
 DT Human Fv molecule hypervariable region related peptide #26.
 DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
 XX Homo sapiens.
 OS WO200259264-A2.
 PN 01-AUG-2002.
 XX 31-DEC-2001; 2001WO-US049440.
 PF 29-DEC-2000; 2000US-00751181.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 PI Plaksin D, Peretz T;
 XX WPI: 2002-619166/66.
 DR N-PSDB; ABS63405.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 PT or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

XX Claim 109; Page 93-94; 232pp; English.
 XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX SQ Sequence 464 AA;
 Query Match 100.0%; Score 29; DB 5; Length 464;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 118 MRAPVI 123

RESULT 27
 ABG92021
 ID ABG92021 standard; protein; 464 AA.
 XX AC ABG92021;
 XX 04-DEC-2002 (first entry)
 DT Antibody protein #1.
 DE Antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX Unidentified.
 OS WO200253700-A2.
 PN 11-JUL-2002.
 XX 31-DEC-2001; 2001WO-US049442.
 PF 29-DEC-2000; 2000US-00751181.
 XX 29-DEC-2000; 2000US-0258948P.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 XX WPI: 2002-674776/72.
 DR N-PSDB; ABS67759.
 XX Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 XX Example 5; Fig 48A; Opp; English.
 PS The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-

CC protein interactions. This sequence represents an antibody protein of the
CC invention
XX
SQ Sequence 464 AA;
Query Match 100.0%; Score 29; DB 5; Length 464;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 118 MRAPVI 123
RESULT 28
ABG91842
ID ABG91842 standard; protein; 464 AA.
XX
AC ABG91842;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human antibody fragment #26.
XX
KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX
OS Homo sapiens.
XX
PN WO200253700-A2.
XX
PD 11-JUL-2002.
XX
PF 31-DEC-2001; 2001WO-US049442.
XX
PR 29-DEC-2000; 2000US-00751181.
PR 29-DEC-2000; 2000US-0258948P.
XX
PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX
PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX
DR WPI; 2002-674776/72.
XX
PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX
PS Disclosure; Page 234-235; Opp; English.
XX
CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet

CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX
SQ Sequence 464 AA;
Query Match 100.0%; Score 29; DB 5; Length 464;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 118 MRAPVI 123
RESULT 29
AAU42688
ID AAU42688 standard; protein; 133 AA.
XX
AC AAU42688;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #3584.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59518.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Example 1; SEQ ID NO 3883; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for

CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 133 AA;
Query Match 96.6%; Score 28; DB 4; Length 133;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
Db 59 MRAPII 64

RESULT 30

ABM39207
ID ABM39207 standard; protein; 133 AA.

XX AC ABM39207;

XX DT 20-OCT-2003 (first entry)

XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #3883.

XX KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

XX KW Immunostimulant; immune response; vaccine.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-) CORIXA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;

XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

XX PI Barth B, Valliave-Douglas J;

XX DR WPI; 2003-381789/36.

XX DR N-PSDB; ACF64447.

XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
PT or for stimulating an immune response specific for a P. acnes protein.

XX PS Example 1; SEQ ID NO 3883; 1481pp; English.

XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
CC encoding a Propionibacterium acnes protein. The invention also relates to
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
CC immunogenic fragments of P. acnes polypeptides. The invention
CC additionally encompasses expression vectors and host cells comprising a
CC polynucleotide of the invention; antibodies against polypeptides of the
CC invention; fusion proteins comprising a polypeptide of the invention; a
CC method for stimulating an immune response specific for a P. acnes
CC polypeptide and an isolated T cell population comprising T cells prepared
CC via this method; a vaccine composition (comprising P. acnes polypeptides,
CC polynucleotides, antibodies, fusion proteins, T cell populations, or
CC antigen-presenting cells that express the polypeptide); a method and kit
CC for detecting or determining the presence or absence of P. acnes in a
CC patient; and a method for inhibiting the development of P. acnes in a
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the

CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 133 AA;

Query Match 96.6%; Score 28; DB 6; Length 133;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||

Db 59 MRAPII 64

RESULT 31

AAE14569

ID AAE14569 standard; protein; 438 AA.

XX AC AAE14569;

XX DT 17-MAY-2002 (first entry)

XX DE Human rhomboid related protein, RRP1.

XX KW Human; rhomboid related protein; RRP1; transmembrane protein;

XX KW epidermal growth factor receptor; EGFR signalling pathway;

XX KW tissue growth factor alpha; TGFalpha; epidermal growth factor; EGF;

XX KW amphiregulin; tumour; p21; cancer; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 239..396

XX FT /label= Rhomboid_domain

XX WO200205843-A2.

XX PD 24-JAN-2002.

XX PF 18-JUL-2001; 2001WO-US022555.

XX PR 19-JUL-2000; 2000US-0219289P.

XX PR 21-MAR-2001; 2001US-0277471P.

XX PR 21-MAR-2001; 2001US-0277487P.

XX PR 12-JUL-2001; 2001US-0304863P.

XX PA (EXEL-) EXELIXIS INC.

XX PI Friedman L, Larson JS, Belvin M, Cheh C, Robertson SA, Lioubin M;

XX PI Shi W, Chan J, Li D;

XX DR WPI; 2002-179749/23.

XX DR N-PSDB; AAD24225.

XX PT Human rhomboid related proteins involved in epidermal growth factor
PT receptor signaling pathway, useful for screening compounds modulating
PT interaction between the protein and binding target, and for inhibiting
PT growth of tumors.

XX PS Disclosure; Page 31-32; 36pp; English.

XX CC The invention relates to human rhomboid related proteins (RRPs) which are
CC transmembrane proteins involved in epidermal growth factor receptor
CC (EGFR) signalling pathway. The polypeptide of the invention is useful for
CC screening agents that modulate the interaction of RRP with an RRP binding
CC target (e.g. tissue growth factor (TGF)alpha, epidermal growth factor
CC (EGF), and amphiregulin). The RRP modulating agent is an antibody or a
CC small organic molecule which can be used to specifically inhibit growth

CC of tumour cells that overexpress an RRP protein. The RRP are important
 CC drug targets for the treatment of pathologies associated with a defective
 CC p21 signalling pathway, e.g. cancer. RRP polynucleotide is useful for
 CC diagnosing a tumour cell, in gene therapy, in genetic studies to
 CC elucidate the EGR pathway, and in animal models of disease and disorders
 CC implicating defective EGR pathway function. The polynucleotide is also
 CC useful as translatable transcripts, hybridisation probes and PCR primers.
 CC The hybridisation probes are used for identifying wild-type and mutant
 CC alleles in clinical and laboratory samples. Mutant alleles are used to
 CC generate allele-specific oligonucleotide (ASO) probes for high-throughput
 CC clinical diagnoses. The present sequence is human RRP1 protein
 XX

SQ Sequence 438 AA;

Query Match 96.6%; Score 28; DB 5; Length 438;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||:
 Db 304 MRAPV 309

RESULT 32
 ADA13449
 ID ADA13449 standard; protein; 438 AA.

XX ADA13449;

XX 20-NOV-2003 (first entry)

DE Human rhomboid related protein RRP1 sequence SEQ ID NO:36.

XX tumour; growth inhibition; rhomboid related protein; RRP; p53; p21;
 KW cytosolic; gene therapy; human.

XX Homo sapiens.

XX WO2003070771-A1.

XX 28-AUG-2003.

XX 22-JAN-2003; 2003WO-US001858.

XX 23-JAN-2002; 2002US-00056790.

XX (EXEL-) EXELIXIS INC.

XX Francis-Lang H, Friedman L, Belvin M, Plowman GD, Larson JS;
 PI Chen C, Robertson SA, Lioubin MN, Shi W, Chan J, Funke RP, Li D;
 PI Kauselmann G, Tintrop H, Zevnik B, Schoor M, Reardon BJ;

XX WPI; 2003-663850/62.

XX Specifically inhibiting the growth of tumor cells that overexpress a
 PT Rhomboid Related Protein (RRP) comprises contacting the tumor cells with
 PT an amount of an exogenous RRP binding agent (e.g. an antibody) to inhibit
 PT tumor growth.

PS Disclosure; Page 99-101; 146pp; English.

XX The present invention describes a method of specifically inhibiting
 CC growth of tumour cells that over-express a rhomboid related protein (RRP)
 CC comprising contacting the tumour cells with an amount of an exogenous RRP
 CC binding agent that results in the inhibition of growth of tumour cells.
 CC Also described: (1) screening for agents that modulate the interaction of
 CC an RRP polypeptide with an RRP binding target; (2) diagnosing a tumour
 CC cell as having abnormal p53 or p21 pathway signaling; (3) identifying a
 CC candidate p53 or p21 pathway modulating agent; (4) modulating a p53 or
 CC p21 pathway of a cell; (5) diagnosing a disease in a patient; (6) a
 CC purified nucleic acid molecule that encodes a RRP polypeptide, or its
 CC reverse complement; (7) a recombinant expression system comprising a DNA
 CC or RNA molecule, where the expression system is capable of producing an

CC MRP1 polypeptide when the expression system is present in a compatible
 CC host cell; (8) producing an mRP1 protein; (9) producing a cell which
 CC produces an mRP1 protein; (10) a recombinant host cell comprising the
 CC expression system of (7) or expressing the protein produced by method (8)
 CC ; (11) a transgenic mouse whose genome comprises a disruption in an
 CC endogenous RRP gene, where the disruption results in decreased expression
 CC or a lack of expression of the endogenous RRP gene; (12) a cell isolated
 CC from the transgenic mouse or whose genome comprises a disruption in an
 CC endogenous RRP gene, where the disruption results in decreased expression
 CC or a lack of expression of the endogenous RRP gene; (13) selecting an
 CC agent that modulates cell proliferation; and (14) making an antibody
 CC against a human RRP. RRP sequences have cytosolic activity, and can be
 CC used in gene therapy. The method of the invention is useful in diagnosing
 CC or specifically inhibiting the growth of tumour cells that over-express
 CC an RRP protein. The RRP nucleic acid and polypeptide sequences can be
 CC used for identifying and testing agents that modulate RRP function and
 CC for other applications related to the involvement of RRP in the p53 or
 CC p21 pathways. The present sequence represents a human RRP1 amino acid
 CC sequence, from the present invention.

XX Sequence 438 AA;

Query Match 96.6%; Score 28; DB 7; Length 438;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 |||||:
 Db 304 MRAPV 309

RESULT 33
 ADA13415

ID ADA13415 standard; protein; 438 AA.

XX ADA13415;

XX 20-NOV-2003 (first entry)

XX Human rhomboid related protein RRP1 SEQ ID NO:2.

XX tumour; growth inhibition; rhomboid related protein; RRP; p53; p21;

KW cytosolic; gene therapy; human.

XX Homo sapiens.

XX WO2003070771-A1.

XX 28-AUG-2003.

XX 22-JAN-2003; 2003WO-US001858.

XX 23-JAN-2002; 2002US-00056790.

XX (EXEL-) EXELIXIS INC.

XX Francis-Lang H, Friedman L, Belvin M, Plowman GD, Larson JS;
 PI Chen C, Robertson SA, Lioubin MN, Shi W, Chan J, Funke RP, Li D;
 PI Kauselmann G, Tintrop H, Zevnik B, Schoor M, Reardon BJ;

XX WPI; 2003-663850/62.

DR N-PSDB; ADA13414.

XX Specifically inhibiting the growth of tumor cells that overexpress a
 PT Rhomboid Related Protein (RRP) comprises contacting the tumor cells with
 PT an amount of an exogenous RRP binding agent (e.g. an antibody) to inhibit
 PT tumor growth.

PS Claim 26; Page 63-65; 146pp; English.

XX The present invention describes a method of specifically inhibiting
 CC growth of tumour cells that over-express a rhomboid related protein (RRP)
 CC comprising contacting the tumour cells with an amount of an exogenous RRP

CC binding agent that results in the inhibition of growth of tumour cells.
 CC Also described: (1) screening for agents that modulate the interaction of
 CC an RRP polypeptide with an RRP binding target; (2) diagnosing a tumour
 CC cell as having abnormal p53 or p21 pathway signaling; (3) identifying a
 CC candidate p53 or p21 pathway modulating agent; (4) modulating a p53 or
 CC p21 pathway of a cell; (5) diagnosing a disease in a patient; (6) a
 CC purified nucleic acid molecule that encodes a RRP polypeptide, or its
 CC reverse complement; (7) a recombinant expression system comprising a DNA
 CC or RNA molecule, where the expression system is capable of producing an
 CC mRNP1 polypeptide when the expression system is present in a compatible
 CC host cell; (8) producing an mRNP1 protein; (9) producing a cell which
 CC produces an mRNP1 protein; (10) a recombinant host cell comprising the
 CC expression system of (7) or expressing the protein produced by method (8)
 CC ; (11) a transgenic mouse whose genome comprises a disruption in an
 CC endogenous RRP gene, where the disruption results in decreased expression
 CC or a lack of expression of the endogenous RRP gene; (12) a cell isolated
 CC from the transgenic mouse or whose genome comprises a disruption in an
 CC endogenous RRP gene, where the disruption results in decreased expression
 CC or a lack of expression of the endogenous RRP gene; (13) selecting an
 CC agent that modulates cell proliferation; and (14) making an antibody
 CC against a human RRP. RRP sequences have cytostatic activity, and can be
 CC used in gene therapy. The method of the invention is useful in diagnosing
 CC or specifically inhibiting the growth of tumour cells that over-express
 CC an RRP protein. The RRP nucleic acid and polypeptide sequences can be
 CC used for identifying and testing agents that modulate RRP function and
 CC for other applications related to the involvement of RRP in the p53 or
 CC p21 pathways. The present sequence represents human RRP1, from the
 CC present invention.

XX Sequence 438 AA;

Query Match 96.6%; Score 28; DB 7; Length 438;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6
 |||||:
 Db 304 MRAPV1 309

RESULT 34

ADG47134
 ID ADG47134 standard; protein; 438 AA.

XX AC ADG47134;

XX 11-MAR-2004 (first entry)

XX Human rhomboid related protein 1 (RRP) #2.

XX RRP; rhomboid related protein; p53; p21; therapy; tumour; breast; ovary;
 KW lung; kidney; colon; human.

XX Homo sapiens.

XX US2003165497-A1.

XX 04-SEP-2003.

XX 23-JAN-2002; 2002US-00056790.

XX 19-JUL-2000; 2000US-0219289P.

XX 21-MAR-2001; 2001US-0277471P.

XX 21-MAR-2001; 2001US-0277487P.

XX 05-JUN-2001; 2001US-0296076P.

XX 12-JUL-2001; 2001US-0304863P.

XX 12-JUL-2001; 2001US-0305017P.

XX 18-JUL-2001; 2001US-0090841P.

XX 10-OCT-2001; 2001US-0328491P.

XX 10-OCT-2001; 2001US-0328605P.

XX (LJOU/) LIOUBIN M N.

XX (FRIE/) FRIEDMAN L.

(BELV/) BELVIN M.
 (LARS/) LARSON J S.
 (CHEN/) CHEN C.
 (ROBE/) ROBERTSON S A.
 (SHIW/) SHI W.
 (CHAN/) CHAN J.
 (LIDD/) LI D.
 (FRAN/) FRANCIS-LANG H.
 (PLOW/) PLOWMAN G D.
 (FUNK/) FUNKE R P.
 (SCHO/) SCHOOR M.
 (ZEVN/) ZEVIK B.
 (KAUS/) KAUSELMANN G.
 (TINT/) TINTRUP H.

LIUBIN MN, Friedman L, Belvin M, Larson JS, Chen C;
 Robertson SA, Shi W, Chan J, Li D, Francis-Lang H, Plowman GD;
 Funke RP, Schoor M, Zevnik B, Kauselmann G, Tinttrup H;

WPI; 2003-898032/82.
 N-PSDB; ADG47116.

Inhibition of growth of tumor cells overexpressing rhomboid related
 protein, RRP, useful therapeutically to inhibit growth of e.g. breast
 tumor cells by contacting with exogenous agent binding a RRP.

Disclosure; SEQ ID NO 36; 84pp; English.

The present invention relates to growth of tumour cells overexpressing a
 rhomboid related protein (RRP) which can be inhibited by contacting an
 exogenous agent binding RRP, since RRP genes are modulators of the p53 or
 p21 pathway. The invention is useful therapeutically to inhibit growth of
 tumour cells overexpressing RRP especially from breast, ovary, lung,
 kidney or colon. The invention is useful to identify agents which can
 modulate and restore p53 or p21 and/or RRP activity. The present sequence
 is human rhomboid related protein 1.

Sequence 438 AA;

Query Match 96.6%; Score 28; DB 7; Length 438;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV1 6
 |||||:
 Db 304 MRAPV1 309

RESULT 35

ADG47100

ID ADG47100 standard; protein; 438 AA.

XX AC ADG47100;

XX 11-MAR-2004 (first entry)

XX Human rhomboid related protein 1 (RRP) #1.

XX RRP; rhomboid related protein; p53; p21; therapy; tumour; breast; ovary;
 KW lung; kidney; colon; human.

XX Homo sapiens.

XX US2003165497-A1.

XX 04-SEP-2003.

XX 23-JAN-2002; 2002US-00056790.

XX 19-JUL-2000; 2000US-0219289P.

XX 21-MAR-2001; 2001US-0277471P.

XX 21-MAR-2001; 2001US-0277487P.

XX 05-JUN-2001; 2001US-0296076P.

```

PR 12-JUL-2001; 2001US-0304863P.
PR 12-JUL-2001; 2001US-0305017P.
PR 18-JUL-2001; 2001US-00908419.
PR 10-OCT-2001; 2001US-0328491P.
PR 10-OCT-2001; 2001US-0328605P.
XX
PA (LIYOU/) LIOUBIN M N.
PA (FRIE/) FRIEDMAN L.
PA (BELV/) BELVIN M.
PA (LARS/) LARSON J S.
PA (CHEN/) CHEN C.
PA (ROBE/) ROBERTSON S A.
PA (SHIW/) SHI W.
PA (CHAN/) CHAN J.
PA (LIDD/) LI D.
PA (FRAN/) FRANCIS-LANG H.
PA (FLOW/) FLOWMAN G D.
PA (FUNK/) FUNK R P.
PA (SCHO/) SCHOOR M.
PA (ZEVI/) ZEVIK B.
PA (KAUS/) KAUSELMANN G.
PA (TINT/) TINTRUP H.
XX
PI Lioubin MN, Friedman L, Belvin M, Larson JS, Chen C;
PI Robertson SA, Shi W, Chan J, Li D, Francis-Lang H, Plowman GD;
PI Funke RP, Schoor M, Zevnik B, Kauselmann G, Tintrup H;
XX
DR WPI; 2003-898032/82.
DR N-PSDB; ADG47099.
XX
PT Inhibition of growth of tumor cells overexpressing rhomboid related
PT protein, RRP, useful therapeutically to inhibit growth of e.g. breast
PT tumor cells by contacting with exogenous agent binding a RRP.
XX
PS Claim 26; SEQ ID NO 2; 84pp; English.
XX
CC The present invention relates to growth of tumor cells overexpressing a
CC rhomboid related protein (RRP) which can be inhibited by contacting an
CC exogenous agent binding RRP, since RRP genes are modulators of the p53 or
CC p21 pathway. The invention is useful therapeutically to inhibit growth of
CC tumor cells overexpressing RRP especially from breast, ovary, lung,
CC kidney or colon. The invention is useful to identify agents which can
CC modulate and restore p53 or p21 and/or RRP activity. The present sequence
CC is human rhomboid related protein 1.
XX
SQ Sequence 438 AA;
Query Match 96.6%; Score 28; DB 7; Length 438;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 304 MRAPVV 309
|||||:
RESULTS 36
ADAL13459
ID ADAL13459 standard; protein; 470 AA.
XX
AC ADAL13459;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse rhomboid related protein RRP1 SEQ ID NO:46.
XX
KW tumour; growth inhibition; rhomboid related protein; RRP; p53; p21;
KW cytostatic; gene therapy; mouse.
XX
OS Mus musculus.
XX
PN WO2003070771-A1.
XX
PR 28-AUG-2003.
XX
PF 22-JAN-2003; 2003WO-US001858.
XX
PR 23-JAN-2002; 2002US-00056790.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Friedman L, Belvin M, Plowman GD, Larson JS;
PI Chen C, Robertson SA, Lioubin MN, Shi W, Chan J, Funke RP, Li D;
PI Kauselmann G, Tintrup H, Zevnik B, Schoor M, Reardon BJ;
XX
DR WPI; 2003-663850/62.
DR N-PSDB; ADAL13458.
XX
PT Specifically inhibiting the growth of tumor cells that overexpress a
PT Rhomboid Related Protein (RRP) comprises contacting the tumor cells with
PT an amount of an exogenous RRP binding agent (e.g. an antibody) to inhibit
PT tumor growth.
XX
PS Claim 26; Page 117-118; 146pp; English.
XX
CC The present invention describes a method of specifically inhibiting
CC growth of tumor cells that over-express a rhomboid related protein (RRP)
CC comprising contacting the tumor cells with an amount of an exogenous RRP
CC binding agent that results in the inhibition of growth of tumor cells.
CC Also described: (1) screening for agents that modulate the interaction of
CC an RRP polypeptide with an RRP binding target; (2) diagnosing a tumour
CC cell as having abnormal p53 or p21 pathway signaling; (3) identifying a
CC candidate p53 or p21 pathway modulating agent; (4) modulating a p53 or
CC p21 pathway of a cell; (5) diagnosing a disease in a patient; (6) a
CC purified nucleic acid molecule that encodes a RRP polypeptide, or its
CC reverse complement; (7) a recombinant expression system comprising a DNA
CC or RNA molecule, where the expression system is capable of producing an
CC mRRP1 polypeptide when the expression system is present in a compatible
CC host cell; (8) producing an mRRP1 protein; (9) producing a cell which
CC produces an mRRP1 protein; (10) a recombinant host cell comprising the
CC expression system of (7) or expressing the protein produced by method (8)
CC; (11) a transgenic mouse whose genome comprises a disruption in an
CC endogenous RRP gene, where the disruption results in decreased expression
CC or a lack of expression of the endogenous RRP gene; (12) a cell isolated
CC from the transgenic mouse or whose genome comprises a disruption in an
CC endogenous RRP gene, where the disruption results in decreased expression
CC or a lack of expression of the endogenous RRP gene; (13) selecting an
CC agent that modulates cell proliferation; and (14) making an antibody
CC against a human RRP. RRP sequences have cytostatic activity, and can be
CC used in gene therapy. The method of the invention is useful in diagnosing
CC or specifically inhibiting the growth of tumour cells that over-express
CC an RRP protein. The RRP nucleic acid and polypeptide sequences can be
CC used for identifying and testing agents that modulate RRP function and
CC for other applications related to the involvement of RRP in the p53 or
CC p21 pathways. The present sequence represents mouse RRP1, from the
CC present invention.
XX
SQ Sequence 470 AA;
Query Match 96.6%; Score 28; DB 7; Length 470;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 348 MRAPVV 353
|||||:
RESULTS 37
ADG47144
ID ADG47144 standard; protein; 470 AA.
XX
AC ADG47144;
XX
DT 11-MAR-2004 (first entry)
XX

```


DE Mouse rhomboid related protein 1 (RRP).
XX RRP; rhomboid related protein; p53, p21; therapy; tumour; breast; ovary;
KW lung; kidney; colon; mouse.
XX Mus musculus.
XX OS
XX US2003165497-A1.
XX
XX 04-SEP-2003.
XX
XX 23-JAN-2002; 2002US-00056790.
XX
XX 19-JUL-2000; 2000US-0219289P.
XX 21-MAR-2001; 2001US-0277471P.
XX 21-MAR-2001; 2001US-0277487P.
XX 05-JUN-2001; 2001US-0296076P.
XX 12-JUL-2001; 2001US-0304863P.
XX 12-JUL-2001; 2001US-0305017P.
XX 18-JUL-2001; 2001US-00908419.
XX 10-OCT-2001; 2001US-0328491P.
XX 10-OCT-2001; 2001US-0328605P.
XX
XX (LIQU/) LIQUIN M. N.
XX (FRIE/) FRIEDMAN L.
XX (BELV/) BELVIN M.
XX (LARS/) LARSON J. S.
XX (CHEN/) CHEN C.
XX (ROBE/) ROBERTSON S. A.
XX (SHIW/) SHI W.
XX (CHAN/) CHAN J.
XX (LIDD/) LI D.
XX (FRAN/) FRANCIS-LANG H.
XX (PLOW/) PLOWMAN G. D.
XX (FUNK/) FUNKE R. P.
XX (SCHG/) SCHOOR M.
XX (ZEVI/) ZEVNIK B.
XX (KAUS/) KAUSELMANN G.
XX (TINT/) TINTRUP H.
XX
XX Lioubin MN, Friedman L, Belvin M, Larson JS, Chen C;
PI Robertson SA, Shi W, Chan J, Li D, Francis-Lang H, Plowman GD;
PI Funke RP, Schoor M, Zevnik B, Kauselmann G, Tintrup H;
XX
XX WPI; 2003-898032/82.
XX N-PSDB; ADG47143.
XX
XX Inhibition of growth of tumor cells overexpressing rhomboid related
PT protein, RRP, useful therapeutically to inhibit growth of e.g. breast
PT tumor cells by contacting with exogenous agent binding a RRP.
XX
XX Claim 26; SEQ ID NO 46; 84pp; English.
XX
XX The present invention relates to growth of tumour cells overexpressing a
CC rhomboid related protein (RRP) which can be inhibited by contacting an
CC exogenous agent binding RRP, since RRP genes are modulators of the p53 or
CC p21 pathway. The invention is useful therapeutically to inhibit growth of
CC tumour cells overexpressing RRP especially from breast, ovary, lung,
CC kidney or colon. The invention is useful to identify agents which can
CC modulate and restore p53 or p21 and/or RRP activity. The present sequence
CC is mouse RRP1.
XX
XX Sequence 470 AA;
SQ

Query Match 96.6%; Score 28; DB 7; Length 470;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 348 MRAPV 353

RESULT 38
AAG90242
ID AAG90242 standard; protein; 541 AA.
XX
XX AAG90242;
AC
XX 26-SEP-2001 (first entry)
DT
XX
DE C glutamicum protein fragment SEQ ID NO: 3996.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis.
XX
OS Corynebacterium glutamicum.
XX
XX EP1108790-A2.
PN
XX 20-JUN-2001.
PD
XX 18-DEC-2000; 2000EP-00127688.
PF
XX 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX N-PSDB; AAH65461.
XX
XX Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene, and identifying homologous gene.
XX
XX Claim 17; SEQ ID NO 3996; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and analysing
CC the expression profile or expression pattern of a gene derived from
CC Coryneform bacterium, and identifying a homologue of a gene derived from
CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
CC acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a protein described in the
CC exemplification of the invention. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the European Patent Office
XX
XX Sequence 541 AA;
SQ

Query Match 96.6%; Score 28; DB 4; Length 541;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 103 MRAPV 108

RESULT 39
ABO75198
ID ABO75198 standard; protein; 973 AA.
XX
XX ABO75198;
AC
XX 29-JUL-2004 (first entry)
DT
XX
DE Pseudomonas aeruginosa polypeptide #7373.
XX

KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
DR N-PSDB; ABD08769.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 23944; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX
SQ Sequence 973 AA;
Query Match 96.6%; Score 28; DB 7; Length 973;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 387 MRAPV 392
|||||:
RESULT 40
AAU44808
ID AAU44808 standard; protein; 116 AA.
XX
XX AAU44808;
XX
XX 27-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein #5704.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
OS
XX
PN WO200101581-A2.
XX

PD 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
PA
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59524.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 6003; 1069pp; English.
PS
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 116 AA;
Query Match 93.1%; Score 27; DB 4; Length 116;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 109 MRAPV 114
|||||:
Search completed: November 18, 2005, 21:08:06
Job time : 82.7143 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:02:00 ; Search time 19,0714 Seconds
(without alignments)
26.010 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 NRAPVI 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCRU COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	96.6	438	2	US-09-908-419-2
2	28	96.6	973	2	US-09-252-991A-23944
3	26	89.7	229	2	US-09-248-796A-16460
4	26	89.7	286	2	US-09-711-164-385
5	26	89.7	350	2	US-09-138-452A-643
6	26	89.7	350	2	US-09-438-185A-605
7	26	89.7	477	2	US-09-489-039A-8906
8	25	86.2	119	2	US-09-252-991A-28425
9	25	86.2	120	2	US-09-107-532A-6688
10	25	86.2	197	2	US-09-902-540-13013
11	25	86.2	222	2	US-09-489-039A-8244
12	25	86.2	222	2	US-09-538-092-272
13	25	86.2	223	2	US-09-134-000C-6010
14	25	86.2	224	2	US-09-538-092-617
15	25	86.2	233	2	US-09-489-039A-7366
16	25	86.2	239	2	US-09-328-352-5866
17	25	86.2	291	2	US-09-602-777A-36
18	25	86.2	359	2	US-09-252-991A-19964
19	25	86.2	398	2	US-09-712-363-160
20	25	86.2	417	2	US-09-270-767-44567
21	25	86.2	459	2	US-09-252-991A-26783
22	25	86.2	481	2	US-09-489-039A-10515
23	25	86.2	487	2	US-09-583-110-3569
24	25	86.2	488	2	US-09-107-433-3552
25	25	86.2	657	2	US-09-252-991A-27682
26	25	86.2	885	2	US-09-902-540-13431
27	25	86.2	962	2	US-09-328-352-7942

28	24	82.8	73	2	US-09-621-976-6392	Sequence 6392, Ap
29	24	82.8	76	2	US-09-636-215-575	Sequence 575, App
30	24	82.8	76	2	US-09-685-166A-575	Sequence 575, App
31	24	82.8	76	2	US-09-685-166A-888	Sequence 888, App
32	24	82.8	76	2	US-09-679-426-575	Sequence 575, App
33	24	82.8	76	2	US-09-679-426-888	Sequence 888, App
34	24	82.8	76	2	US-09-759-143-575	Sequence 575, App
35	24	82.8	76	2	US-09-759-143-888	Sequence 888, App
36	24	82.8	76	2	US-09-651-236-575	Sequence 575, App
37	24	82.8	76	2	US-09-657-279-575	Sequence 575, App
38	24	82.8	76	2	US-10-012-896-575	Sequence 575, App
39	24	82.8	76	2	US-10-012-896-888	Sequence 888, App
40	24	82.8	76	2	US-09-134-001C-4676	Sequence 4676, App
41	24	82.8	82	2	US-09-134-001C-4563	Sequence 4563, App
42	24	82.8	93	2	US-09-938-806A-8	Sequence 8, Appli
43	24	82.8	102	2	US-09-248-796A-14433	Sequence 14433, A
44	24	82.8	108	2	US-09-513-999C-5944	Sequence 5944, Ap
45	24	82.8	125	2	US-09-199-637A-403	Sequence 403, App
46	24	82.8	125	2	US-09-269-410-11	Sequence 11, Appl
47	24	82.8	125	2	US-09-513-999C-5838	Sequence 5838, Ap
48	24	82.8	142	2	US-10-104-047-3548	Sequence 3548, Ap
49	24	82.8	143	2	US-09-270-767-42631	Sequence 42631, A
50	24	82.8	162	2	US-08-801-742-3	Sequence 3, Appli
51	24	82.8	192	1	US-08-208-008C-9	Sequence 9, Appli
52	24	82.8	196	2	US-09-949-016-8609	Sequence 8609, Ap
53	24	82.8	220	2	US-09-489-039A-8353	Sequence 8353, Ap
54	24	82.8	227	2	US-09-902-540-15523	Sequence 15523, A
55	24	82.8	228	2	US-09-605-703B-1202	Sequence 1202, Ap
56	24	82.8	228	2	US-09-605-703B-1204	Sequence 1204, Ap
57	24	82.8	247	1	US-07-885-089B-2	Sequence 2, Appli
58	24	82.8	247	1	US-07-885-089B-8	Sequence 8, Appli
59	24	82.8	252	1	US-07-885-089B-7	Sequence 7, Appli
60	24	82.8	252	2	US-09-976-594-582	Sequence 582, App
61	24	82.8	252	2	US-09-919-039-228	Sequence 228, App
62	24	82.8	253	2	US-09-134-001C-5435	Sequence 5435, Ap
63	24	82.8	253	2	US-09-710-279-2218	Sequence 2218, Ap
64	24	82.8	269	2	US-09-252-991A-31653	Sequence 31653, A
65	24	82.8	271	2	US-09-902-540-15639	Sequence 15639, A
66	24	82.8	292	2	US-09-710-279-2814	Sequence 2814, Ap
67	24	82.8	292	2	US-09-710-279-3034	Sequence 3034, Ap
68	24	82.8	297	2	US-09-902-540-12237	Sequence 12237, A
69	24	82.8	322	2	US-09-949-016-11381	Sequence 11381, A
70	24	82.8	324	2	US-09-489-039A-11252	Sequence 11252, A
71	24	82.8	338	2	US-09-949-016-5950	Sequence 5950, Ap
72	24	82.8	356	2	US-09-134-001C-3408	Sequence 3408, Ap
73	24	82.8	363	2	US-08-912-560-2	Sequence 2, Appli
74	24	82.8	408	2	US-09-949-016-8111	Sequence 8111, Ap
75	24	82.8	409	1	US-08-403-545-2	Sequence 2, Appli
76	24	82.8	409	2	US-08-404-381-2	Sequence 2, Appli
77	24	82.8	410	2	US-09-258-754-451	Sequence 451, App
78	24	82.8	410	2	US-09-676-475A-451	Sequence 451, App
79	24	82.8	411	2	US-09-258-754-448	Sequence 448, App
80	24	82.8	411	2	US-09-676-475A-448	Sequence 448, App
81	24	82.8	412	2	US-09-902-540-15137	Sequence 15137, A
82	24	82.8	429	2	US-09-252-991A-30995	Sequence 30995, A
83	24	82.8	453	2	US-09-543-681A-5855	Sequence 5855, Ap
84	24	82.8	461	2	US-09-489-039A-8460	Sequence 8460, Ap
85	24	82.8	464	2	US-09-252-991A-16660	Sequence 16660, A
86	24	82.8	466	2	US-09-248-796A-15591	Sequence 15591, A
87	24	82.8	478	2	US-09-902-540-15914	Sequence 15914, A
88	24	82.8	478	2	US-09-273-871A-3	Sequence 3, Appli
89	24	82.8	478	2	US-10-083-452-3	Sequence 3, Appli
90	24	82.8	495	2	US-09-273-871A-2	Sequence 2, Appli
91	24	82.8	495	2	US-10-083-452-2	Sequence 2, Appli
92	24	82.8	564	2	US-09-809-665A-30	Sequence 30, Appl
93	24	82.8	568	2	US-09-543-681A-6966	Sequence 6966, Ap
94	24	82.8	580	2	US-09-198-452A-609	Sequence 609, App
95	24	82.8	582	2	US-09-438-185A-572	Sequence 572, App
96	24	82.8	614	2	US-09-252-991A-20060	Sequence 20060, A
97	24	82.8	699	2	US-09-248-796A-23200	Sequence 23200, A
98	24	82.8	701	2	US-09-370-368-10	Sequence 10, Appl
99	24	82.8	919	2	US-09-437-054A-17	Sequence 17, Appl
100	24	82.8	936	2	US-09-252-991A-30190	Sequence 30190, A

```
ALIGNMENTS

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16460
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16460

Query Match      89.7%; Score 26; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      182 MKAPVI 187

RESULT 4
US-09-711-164-385
; Sequence 385, Application US/097111164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Alllyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-385

Query Match      89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      41 MRSPVI 46

RESULT 5
US-09-198-452A-643
; Sequence 643, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 643
; LENGTH: 350

US-09-908-419-2
; Sequence 2, Application US/09908419
; Patent No. 6924117
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: HUMAN RRP SEQUENCES AND METHODS OF USE
; FILE REFERENCE: EX01-041C
; CURRENT APPLICATION NUMBER: US/09/908,419
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,471
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-419-2

Query Match      96.6%; Score 28; DB 2; Length 438;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      304 MRAPV 309

RESULT 2
US-09-252-991A-23944
; Sequence 23944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23944
; LENGTH: 973
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23944

Query Match      96.6%; Score 28; DB 2; Length 973;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      387 MRAPV 392

RESULT 3
US-09-248-796A-16460
; Sequence 16460, Application US/09248796A
; Patent No. 6747137
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TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-643

Query Match 89.7%; Score 26; DB 2; Length 350;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
:|||||
DB 109 LRAPVI 114

RESULT 6

US-09-438-185A-605
Sequence 605, Application US/09438185A
Patent No. 6822071
GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 605
LENGTH: 350
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPN0603
US-09-438-185A-605

Query Match 89.7%; Score 26; DB 2; Length 350;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
:|||||
DB 109 LRAPVI 114

RESULT 7

US-09-489-039A-8906
Sequence 8906, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8906
LENGTH: 477
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8906

Query Match 89.7%; Score 26; DB 2; Length 477;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
:|||||
DB 269 MKAPVI 274

RESULT 8

US-09-252-991A-28425
Sequence 28425, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28425
LENGTH: 119
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28425

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPVI 6
:|||||
DB 63 MRAPTI 68

RESULT 9

US-09-107-532A-6688
Sequence 6688, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

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/ INFORMATION FOR SEQ ID NO: 6688:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 120 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/   ORGANISM: Enterococcus faecium
/ FEATURE:
/   NAME/KEY: misc_feature
/   LOCATION: (B) LOCATION 1...120
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6688:
US-09-107-532A-6688

Query Match      86.2%; Score 25; DB 2; Length 120;
Best Local Similarity 56.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 6
Db      17 MKAPII 22

RESULT 10
US-09-902-540-13013
; Sequence 13013, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13013
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13013

Query Match      86.2%; Score 25; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 5
Db      1 MRAPV 5

RESULT 11
US-09-489-039A-8244
; Sequence 8244, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8244
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
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US-09-489-039A-8244

Query Match      86.2%; Score 25; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 5
Db      24 MRAPV 28

RESULT 12
US-09-538-092-272
; Sequence 272, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormer Version 0.9
; SEQ ID NO 272
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YFL060C
US-09-538-092-272

Query Match      86.2%; Score 25; DB 2; Length 222;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 6
Db      151 IRAPV 156

RESULT 13
US-09-134-000C-6010
; Sequence 6010, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6010
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6010

Query Match      86.2%; Score 25; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 5
```

```
Db      127 MRAPV 131
|||||
GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5866
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5866

Query Match      86.2%; Score 25; DB 2; Length 239;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
      |:|:|:|:
Db      140 MKAPVV 145

RESULT 17
US-09-602-777A-36
; Sequence 36, Application US/09602777A
; Patent No. 683165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4

US-09-538-092-617
; Sequence 617, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformatter Version 0.9
; SEQ ID NO 617
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR095C
US-09-538-092-617

Query Match      86.2%; Score 25; DB 2; Length 224;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
      |:|:|:|:
Db      160 IRAPVI 165

RESULT 15
US-09-489-039A-7366
; Sequence 7366, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7366
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7366

Query Match      86.2%; Score 25; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPV 5
      |:|:|:|:
Db      173 MRAPV 177

RESULT 16
US-09-328-352-5866
; Sequence 5866, Application US/09328352
; Patent No. 6562958
```

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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 36
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-36

Query Match      86.2%; Score 25; DB 2; Length 291;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      |||||
Db      4 MRAPLV 9

RESULT 18
US-09-252-991A-19964
; Sequence 19964, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19964
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19964

Query Match      86.2%; Score 25; DB 2; Length 359;
Best Local Similarity 66.7%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      :||||
Db      212 LRAPVV 217

RESULT 19
US-09-712-363-160
; Sequence 160, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001

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; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-160

Query Match      86.2%; Score 25; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      |||||
Db      1 MRTPVI 6

RESULT 20
US-09-270-767-44567
; Sequence 44567, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 44567
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44567

Query Match      86.2%; Score 25; DB 2; Length 417;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      :||||
Db      211 LRAPVV 216

RESULT 21
US-09-252-991A-26783
; Sequence 26783, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26783
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26783

Query Match      86.2%; Score 25; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 5
      |||||
Db      38 MRAPV 42

RESULT 22
US-09-489-039A-10515
; Sequence 10515, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10515
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10515

Query Match      86.2%; Score 25; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPV 5
      |||||
Db      131 MRAPV 135

RESULT 23
US-09-583-110-3569
; Sequence 3569, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3569
; LENGTH: 487
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```
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3569

Query Match      86.2%; Score 25; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      :|||:|
Db      48 LRAPVI 53

RESULT 24
US-09-107-433-3552
; Sequence 3552, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-5007
; INFORMATION FOR SEQ ID NO: 3552:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...488
; SEQUENCE DESCRIPTION: SEQ ID NO: 3552:
US-09-107-433-3552

Query Match      86.2%; Score 25; DB 2; Length 488;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRAPVI 6
      :|||:|
Db      49 LRAPVI 54
```

```
RESULT 25
US-09-252-991A-27682
; Sequence 27682, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27682
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27682

Query Match      86.2%; Score 25; DB 2; Length 657;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPV 6
      :||||:
Db      332 LRAPV 337

RESULT 26
US-09-902-540-13431
; Sequence 13431, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13431
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13431

Query Match      86.2%; Score 25; DB 2; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPV 5
      :||||:
Db      121 MRAPV 125

RESULT 27
US-09-328-352-7942
; Sequence 7942, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Berton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
```

```
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7942
; LENGTH: 962
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7942

Query Match      86.2%; Score 25; DB 2; Length 962;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MRAPV 6
      :||||:
Db      471 MRAPV 476

RESULT 28
US-09-621-976-6392
; Sequence 6392, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6392
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6392

Query Match      82.8%; Score 24; DB 2; Length 73;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPV 5
      :||||:
Db      13 MRAPV 17

RESULT 29
US-09-636-215-575
; Sequence 575, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John H.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121-42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
```

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; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RAPVI 6
DB      18 RAPVI 22

RESULT 30
US-09-685-166A-575
; Sequence 575, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RAPVI 6
DB      18 RAPVI 22

RESULT 31
US-09-685-166A-888
; Sequence 888, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RAPVI 6
DB      18 RAPVI 22

RESULT 32
US-09-679-426-575
; Sequence 575, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RAPVI 6
DB      18 RAPVI 22

RESULT 33
US-09-679-426-575
; Sequence 575, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RAPVI 6
DB      18 RAPVI 22
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Db          18 RAPVI 22

; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-575

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 RAPVI 6
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Db          18 RAPVI 22

RESULT 35
US-09-759-143-888
; Sequence 888, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 888
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-888

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 RAPVI 6
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Db          18 RAPVI 22

RESULT 36
US-09-651-236-575
; Sequence 575, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; CURRENT FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-236-575

Query Match 82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 18 RAPVI 22

RESULT 37
US-09-657-279-575
; Sequence 575, Application US/09657279
; Patent No. 6894146
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-657-279-575

Query Match 82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6

Db 18 RAPVI 22

RESULT 38
US-10-012-896-575
; Sequence 575, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 575
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-575

Query Match 82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 18 RAPVI 22

RESULT 39
US-10-012-896-888
; Sequence 888, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun

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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Mesgher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 888
; LENGTH: 76
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; ORGANISM: Homo sapiens
US-10-012-896-888

Query Match      82.8%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RAPVI 6
Db      18 RAPVI 22

RESULT 40
US-09-134-001C-4676
; Sequence 4676, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4676
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4676

Query Match      82.8%; Score 24; DB 2; Length 82;
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Db      67 VRAPVI 72

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Job time : 21.0714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:14:46 ; Search time 64.5 Seconds
(without alignments)
38.868 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPVI 6

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	29	100.0	6	4	US-10-029-988B-8
3	29	100.0	6	4	US-10-032-423A-8
4	29	100.0	6	4	US-10-029-926B-8
5	29	100.0	6	4	US-10-610-843B-4
6	29	100.0	6	4	US-10-611-588C-2
7	29	100.0	6	5	US-10-880-922-4
8	29	100.0	266	4	US-10-032-037B-204
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11	29	100.0	277	4	US-10-032-037B-25
12	29	100.0	277	4	US-10-029-988B-25
13	29	100.0	277	4	US-10-032-423A-25
14	29	100.0	277	4	US-10-029-926B-25
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17	29	100.0	280	4	US-10-610-843B-3
18	29	100.0	280	4	US-10-611-588C-1
19	29	100.0	442	4	US-10-369-493-7871
20	29	100.0	464	4	US-10-032-037B-26
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22	29	100.0	464	4	US-10-032-423A-26
23	29	100.0	464	4	US-10-029-926B-26
24	28	96.6	86	4	US-10-424-599-253048
25	28	96.6	123	4	US-10-424-599-150638
26	28	96.6	343	4	US-10-263-367-12
27	28	96.6	438	3	US-09-908-419-2

28	96.6	438	4	US-10-056-790-2	Sequence 2, Appli
28	96.6	438	4	US-10-056-790-36	Sequence 36, Appl
28	96.6	438	5	US-10-477-505A-11	Sequence 11, Appl
28	96.6	470	4	US-10-056-790-46	Sequence 46, Appl
28	96.6	541	3	US-09-738-626-3996	Sequence 3996, Ap
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33	89.7	74	4	US-10-425-115-294304	Sequence 294304,
34	89.7	112	4	US-10-767-701-42410	Sequence 42410, A
26	89.7	226	4	US-10-032-585-7418	Sequence 7418, Ap
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37	89.7	286	4	US-10-287-274-385	Sequence 385, App
38	89.7	286	4	US-10-369-493-23563	Sequence 23563, A
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41	89.7	288	4	US-10-425-114-69148	Sequence 69148, A
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47	89.7	395	4	US-10-425-115-294306	Sequence 294306,
48	89.7	405	4	US-10-017-161-2090	Sequence 2090, Ap
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55	89.7	1449	6	US-11-097-143-24972	Sequence 24972, A
56	86.2	49	4	US-10-724-972A-3811	Sequence 3811, Ap
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58	86.2	49	4	US-10-724-972A-6317	Sequence 6317, Ap
59	86.2	58	4	US-10-437-963-137085	Sequence 137085,
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61	86.2	63	4	US-10-767-701-48548	Sequence 48548, A
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64	86.2	104	4	US-10-437-963-164399	Sequence 164399,
65	86.2	108	4	US-10-425-115-336776	Sequence 336776,
66	86.2	110	4	US-10-437-963-158848	Sequence 158848,
67	86.2	116	3	US-09-864-408A-2530	Sequence 2530, Ap
68	86.2	133	4	US-10-437-963-181680	Sequence 181680,
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76	86.2	215	4	US-10-156-761-13684	Sequence 13684, A
77	86.2	233	4	US-10-425-115-231625	Sequence 231625,
78	86.2	238	4	US-10-425-114-68969	Sequence 68969, A
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80	86.2	257	4	US-10-425-115-269207	Sequence 269207,
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84	86.2	325	4	US-10-437-963-102977	Sequence 102977,
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86	86.2	334	4	US-10-282-122A-53734	Sequence 53734, A
87	86.2	335	4	US-10-146-772-302	Sequence 302, App
88	86.2	335	4	US-10-241-742-302	Sequence 302, App
89	86.2	335	4	US-10-440-523-302	Sequence 302, App
90	86.2	335	4	US-10-440-503-302	Sequence 302, App
91	86.2	335	4	US-10-461-925-302	Sequence 123550,
92	86.2	358	4	US-10-437-963-123550	Sequence 123550,
93	86.2	358	4	US-10-369-493-499	Sequence 499, App
94	86.2	358	4	US-10-369-493-21248	Sequence 21248, A
95	86.2	365	4	US-10-424-599-235507	Sequence 235507,
96	86.2	366	4	US-10-437-963-175310	Sequence 175310,
97	86.2	394	4	US-10-369-493-7836	Sequence 7836, Ap
98	86.2	398	3	US-09-712-363-160	Sequence 160, App
99	86.2	410	4	US-10-425-114-37988	Sequence 37988, A
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ALIGNMENTS

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RESULT 1
US-10-032-037B-8
; Sequence 8, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-8
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 1 MRAPVI 6

RESULT 2
US-10-029-988B-8
; Sequence 8, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-8
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 1 MRAPVI 6

RESULT 3
US-10-032-423A-8
; Sequence 8, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-8
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 1 MRAPVI 6

RESULT 4
US-10-029-926B-8
; Sequence 8, Application US/10029926B
; Publication No. US200400073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-8
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 1 MRAPVI 6

RESULT 5
US-10-610-843B-4
; Sequence 4, Application US/10610843B
; Publication No. US20040202665A1
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-610-843B-4
Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 1 MRAPVI 6
```


Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
| | | | |
Db 1 MRAPVI 6

RESULT 6

US-10-611-588C-2

; Sequence 2, Application US/10611588C

; Publication No. US20040208877A1

; GENERAL INFORMATION:

; APPLICANT: Levanon, et al.

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793/70

; CURRENT APPLICATION NUMBER: US/10/611,588C

; CURRENT FILING DATE: 2003-06-30

; PRIOR APPLICATION NUMBER: 60/393,491

; PRIOR FILING DATE: 2002-07-01

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-611-588C-2

Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
| | | | |
Db 1 MRAPVI 6

RESULT 7

US-10-880-922-4

; Sequence 4, Application US/10880922

; Publication No. US20050069955A1

; GENERAL INFORMATION:

; APPLICANT: PLAKSIN, DANIEL

; APPLICANT: LEVANON, AVIGDOR

; APPLICANT: SZANTON, ESTHER

; APPLICANT: HAGAY, YOCHVED

; APPLICANT: BEN-LEVY, RACHEL

; APPLICANT: NISGAV, Yael

; APPLICANT: KANFI, YARIV

; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

; FILE REFERENCE: 10793-143

; CURRENT APPLICATION NUMBER: US/10/880,922

; CURRENT FILING DATE: 2004-06-30

; PRIOR APPLICATION NUMBER: 60/484,051

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn ver. 3.2

; SEQ ID NO 4

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-10-880-922-4

Query Match

Best Local Similarity 100.0%; Score 29; DB 5; Length 6;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
| | | | |
Db 1 MRAPVI 6

RESULT 8

US-10-032-037B-204

; Sequence 204, Application US/10032037B

; Publication No. US20040001822A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/44

; CURRENT APPLICATION NUMBER: US/10/032,037B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 204

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-037B-204

Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 266;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
| | | | |
Db 121 MRAPVI 126

RESULT 9

US-10-029-988B-204

; Sequence 204, Application US/10029988B

; Publication No. US20040001839A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/46

; CURRENT APPLICATION NUMBER: US/10/029,988B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 204

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-029-988B-204

Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 266;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
| | | | |
Db 121 MRAPVI 126

RESULT 10

US-10-032-423A-204

; Sequence 204, Application US/10032423A

; Publication No. US20040002450A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

; FILE REFERENCE: 10793/45

; CURRENT APPLICATION NUMBER: US/10/032,423A

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

```
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 204
/ LENGTH: 266
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match      100.0%; Score 29; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      1 MRAPVI 6
Db      121 MRAPVI 126

RESULT 11
US-10-032-037B-25
/ Sequence 25, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032,037B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match      100.0%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      1 MRAPVI 6
Db      121 MRAPVI 126

RESULT 12
US-10-029-988B-25
/ Sequence 25, Application US/10029988B
/ Publication No. US20040001839A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/46
/ CURRENT APPLICATION NUMBER: US/10/029,988B
/ PRIOR FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-988B-25

Query Match      100.0%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      1 MRAPVI 6
Db      121 MRAPVI 126

RESULT 13
US-10-032-423A-25
/ Sequence 25, Application US/10032423A
/ Publication No. US20040002450A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ FILE REFERENCE: 10793/45
/ CURRENT APPLICATION NUMBER: US/10/032,423A
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match      100.0%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      1 MRAPVI 6
Db      121 MRAPVI 126

RESULT 14
US-10-029-926B-25
/ Sequence 25, Application US/10029926B
/ Publication No. US20040073011A1
/ GENERAL INFORMATION:
/ APPLICANT: HAGAV, et al.
/ TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
/ FILE REFERENCE: 10793/50
/ CURRENT APPLICATION NUMBER: US/10/029,926B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 12/29/2000
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 277
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match      100.0%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy      1 MRAPVI 6
Db      121 MRAPVI 126

RESULT 15
US-10-610-843B-1
/ Sequence 1, Application US/10610843B
/ Publication No. US2004020265A1
/ GENERAL INFORMATION:
/ APPLICANT: Lazarovits, et al.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
/ FILE REFERENCE: 10793/72
/ CURRENT APPLICATION NUMBER: US/10/610,843B
```

; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-610-843B-1

Query Match 100.0%; Score 29; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 121 MRAPVI 126

RESULT 16
US-10-610-843B-2
; Sequence 2, Application US/10610843B
; Publication No. US20040202665A1
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-610-843B-2

Query Match 100.0%; Score 29; DB 4; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 122 MRAPVI 127

RESULT 17
US-10-610-843B-3
; Sequence 3, Application US/10610843B
; Publication No. US20040202665A1
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-610-843B-3

Query Match 100.0%; Score 29; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 124 MRAPVI 129

RESULT 18
US-10-611-588C-1
; Sequence 1, Application US/10611588C
; Publication No. US20040208877A1
; GENERAL INFORMATION:
; APPLICANT: Levanon, et al.
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 10793/70
; CURRENT APPLICATION NUMBER: US/10/611,588C
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,491
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-611-588C-1

Query Match 100.0%; Score 29; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 124 MRAPVI 129

RESULT 19
US-10-369-493-7871
; Sequence 7871, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7871
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7871

Query Match 100.0%; Score 29; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 77 MRAPVI 82

RESULT 20
US-10-032-037B-26
; Sequence 26, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-26

Query Match 100.0%; Score 29; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

RESULT 21
US-10-029-988B-26
; Sequence 26, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-26

Query Match 100.0%; Score 29; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

RESULT 22
US-10-032-423A-26
; Sequence 26, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 96.6%; Score 28; DB 4; Length 86;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

US-10-032-423A-26

Query Match 100.0%; Score 29; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

RESULT 23
US-10-029-926B-26
; Sequence 26, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-26

Query Match 100.0%; Score 29; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

RESULT 24
US-10-424-599-253048
; Sequence 253048, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 253048
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max

Query Match 96.6%; Score 28; DB 4; Length 86;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 118 MRAPVI 123

```
Db          1 MRAPV 6

RESULT 25
US-10-424-599-150638
; Sequence 150638, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150638
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107050C.1.pep
US-10-424-599-150638

Query Match          96.6%; Score 28; DB 4; Length 123;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 MRAPV 6
           |||||:
Db          98 MRAPV 103

RESULT 26
US-10-263-367-12
; Sequence 12, Application US/10263367
; Publication No. US20040148644A1
; GENERAL INFORMATION:
; APPLICANT: BIER, ETHAN
; TITLE OF INVENTION: A METHOD FOR GENERATING OVEREXPRESSION OF ALLELES IN
; FILE REFERENCE: 041673-0401
; CURRENT APPLICATION NUMBER: US/10/263,367
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,546
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-367-12

Query Match          96.6%; Score 28; DB 4; Length 343;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 MRAPV 6
           |||||:
Db          209 MRAPV 214

RESULT 27
US-09-908-419-2
; Sequence 2, Application US/09908419
; Patent No. US20020022029A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: HUMAN RRP SEQUENCES AND METHODS OF USE
; FILE REFERENCE: EX01-041C
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; CURRENT APPLICATION NUMBER: US/09/908,419
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,471
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-908-419-2

Query Match          96.6%; Score 28; DB 3; Length 438;
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 MRAPV 6
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Db          304 MRAPV 309

RESULT 28
US-10-056-790-2
; Sequence 2, Application US/10056790
; Publication No. US20030165497A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
; FILE REFERENCE: RRPCIP2002
; CURRENT APPLICATION NUMBER: US/10/056,790
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/908,419
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/277,471
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/304,863
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/305,017
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,491
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-790-2

Query Match          96.6%; Score 28; DB 4; Length 438;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 MRAPV 6
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Db          304 MRAPV 309

RESULT 29
US-10-056-790-36
; Sequence 36, Application US/10056790
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; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3996
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3996

Query Match          96.6%; Score 28; DB 3; Length 541;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      103 MRAPV 108

RESULT 33
US-10-424-599-272558
; Sequence 272558, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272558
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_88141C.1.pep
US-10-424-599-272558

Query Match          93.1%; Score 27; DB 4; Length 99;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      69 MRAPV 74

RESULT 34
US-10-425-115-294304
; Sequence 294304, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 294304
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_31492C.1.pep
US-10-425-115-294304

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US-10-029-926d-8.rapbm

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DB      15 LRAPVI 20

RESULT 35
US-10-767-701-42410
; Sequence 42410, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42410
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C4646_1.pep
US-10-767-701-42410

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QY      1 MRAPVI 6
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RESULT 36
US-10-032-585-7418
; Sequence 7418, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiaang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7418
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7418

Query Match          89.7%; Score 26; DB 4; Length 226;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAPVI 6
DB      179 MRAPVI 184

RESULT 37
US-10-425-115-335198
; Sequence 335198, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 335198
/ LENGTH: 258
/ TYPE: PRT
/ ORGANISM: Zea mays
/ NAME/KEY: unsure
/ LOCATION: (1)...(258)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_68812C.1.pgp
US-10-425-115-335198

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Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6

Db 185 MRAPVM 190

RESULT 38

US-10-287-274-385

/ Sequence 385, Application US/10287274

/ Publication No. US20030181408A1

/ GENERAL INFORMATION:

/ APPLICANT: Forsyth, R. Allyn

/ APPLICANT: Ohlsen, Kari

/ APPLICANT: Zyskind, Judith

/ TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF

/ FILE REFERENCE: ELITRA.08DVI

/ CURRENT APPLICATION NUMBER: US/10/287,274

/ CURRENT FILING DATE: 2002-10-31

/ PRIOR APPLICATION NUMBER: US 60/164415

/ PRIOR FILING DATE: 1999-11-09

/ PRIOR APPLICATION NUMBER: US 09/711164

/ PRIOR FILING DATE: 2000-11-09

/ NUMBER OF SEQ ID NOS: 469

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 385

/ LENGTH: 286

/ TYPE: PRT

/ ORGANISM: Escherichia coli

US-10-287-274-385

Query Match

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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6

Db 41 MRSPVI 46

RESULT 39

US-10-369-493-23563

/ Sequence 23563, Application US/10369493

/ Publication No. US20030233675A1

/ GENERAL INFORMATION:

/ APPLICANT: Cao, Yongwei

/ APPLICANT: Hinkle, Gregory J.

/ APPLICANT: Slater, Steven C.

/ APPLICANT: Goldman, Barry S.

/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 23563
/ LENGTH: 286
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-10-369-493-23563

Query Match 89.7%; Score 26; DB 4; Length 286;

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6

Db 41 MRSPVI 46

RESULT 40

US-10-282-122A-43216

/ Sequence 43216, Application US/10282122A

/ Publication No. US20040029129A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, Liangsu

/ APPLICANT: Zamudio, Carlos

/ APPLICANT: Malone, Cheryl

/ APPLICANT: Hasebeck, Robert

/ APPLICANT: Ohlsen, Kari

/ APPLICANT: Zyskind, Judith

/ APPLICANT: Wall, Daniel

/ APPLICANT: Trawick, John

/ APPLICANT: Carr, Grant

/ APPLICANT: Yamamoto, Robert

/ APPLICANT: Forsyth, R.

/ APPLICANT: Xu, H.

/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

/ FILE REFERENCE: ELITRA.034A

/ CURRENT APPLICATION NUMBER: US/10/282,122A

/ CURRENT FILING DATE: 2003-02-20

/ PRIOR APPLICATION NUMBER: 60/191,078

/ PRIOR FILING DATE: 2000-03-21

/ PRIOR APPLICATION NUMBER: 60/206,848

/ PRIOR FILING DATE: 2000-05-23

/ PRIOR APPLICATION NUMBER: 60/207,727

/ PRIOR FILING DATE: 2000-05-26

/ PRIOR APPLICATION NUMBER: 60/230,335

/ PRIOR FILING DATE: 2000-09-06

/ PRIOR APPLICATION NUMBER: 60/230,347

/ PRIOR FILING DATE: 2000-09-09

/ PRIOR APPLICATION NUMBER: 60/242,578

/ PRIOR FILING DATE: 2000-10-23

/ PRIOR APPLICATION NUMBER: 60/253,625

/ PRIOR FILING DATE: 2000-11-27

/ PRIOR APPLICATION NUMBER: 60/257,931

/ PRIOR FILING DATE: 2000-12-22

/ PRIOR APPLICATION NUMBER: 60/267,636

/ PRIOR FILING DATE: 2001-02-09

/ PRIOR APPLICATION NUMBER: 60/269,308

/ PRIOR FILING DATE: 2001-02-16

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 78614

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 43216

/ LENGTH: 286

/ TYPE: PRT

/ ORGANISM: Escherichia coli

US-10-282-122A-43216

Query Match 89.7%; Score 26; DB 4; Length 286;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
||:|
Db 41 MRSPVI 46

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Job time : 66.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:15:38 ; Search time 1.71429 Seconds
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Perfect score: 29

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Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New.*

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*Pred. No. is the number of results predicted by chance to have a
*score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	22	75.9	103	7	US-11-074-176-286
4	22	75.9	273	1	US-10-467-962B-71
5	22	75.9	308	7	US-11-074-176-308
6	22	75.9	314	7	US-11-074-176-38
7	22	75.9	423	1	US-10-467-962B-85
8	22	75.9	437	1	US-10-967-648A-2
9	22	75.9	439	7	US-11-034-569-16
10	22	75.9	2280	7	US-11-022-562-211
11	21	72.4	12	7	US-11-016-706-10
12	21	72.4	78	1	US-10-986-501-357
13	21	72.4	146	1	US-10-982-545-4
14	21	72.4	416	7	US-11-016-706-38
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35	21	72.4	2280	7	US-11-022-562-211
36	21	72.4	12	7	US-11-016-706-10
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84	21	72.4	439	7	US-11-034-569-16
85	21	72.4	2280	7	US-11-022-562-211
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Sequence 996, Appl
Sequence 998, Appl
Sequence 1000, Appl

99 18 62.1 231 1 US-10-884-730-368 Sequence 368, App
100 18 62.1 231 1 US-10-884-730-369 Sequence 369, App

ALIGNMENTS

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RESULT 1
US-11-109-156-4
; Sequence 4, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-4
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Query Match 82.8%; Score 24; DB 7; Length 865;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
Db 213 MRTPII 218

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RESULT 2
US-10-467-962B-35
; Sequence 95, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
```

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; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 95
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-95
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Query Match 79.3%; Score 23; DB 1; Length 592;
Best Local Similarity 80.0%; Pred. No. 27;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
|||
Db 296 RAPVV 300

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RESULT 3
US-11-074-176-286
; Sequence 286, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-286
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Query Match 75.9%; Score 22; DB 7; Length 103;
Best Local Similarity 66.7%; Pred. No. 6;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||
Db 33 MQSPVI 38

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RESULT 4
US-10-467-962B-71
; Sequence 71, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
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; SOFTWARE: PatentIn Vers. 2.0

; SEQ ID NO 71

; LENGTH: 273

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-467-962B-71

Query Match

Best Local Similarity 75.9%; Score 22; DB 1; Length 273;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5

Db 122 MKAPV 126

RESULT 5

US-11-074-176-308

; Sequence 308, Application US/11074176

; Publication No. US20050250135A1

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAuliffe, Olivia

; APPLICANT: Peril, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

; FILE REFERENCE: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694

; CURRENT FILING DATE: 2005-03-07

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 308

; LENGTH: 308

; TYPE: PRT

; ORGANISM: Lactobacillus acidophilus

US-11-074-176-308

Query Match

Best Local Similarity 75.9%; Score 22; DB 7; Length 308;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAPVI 6

Db 102 RAPVL 106

RESULT 6

US-11-074-176-38

; Sequence 38, Application US/11074176

; Publication No. US20050250135A1

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAuliffe, Olivia

; APPLICANT: Peril, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

; FILE REFERENCE: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694

; CURRENT FILING DATE: 2005-03-07

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 38

; LENGTH: 314

; TYPE: PRT

; ORGANISM: Lactobacillus acidophilus

US-11-074-176-38

Query Match

Best Local Similarity 75.9%; Score 22; DB 7; Length 314;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAPVI 6

Db 108 RAPVL 112

RESULT 7

US-10-467-962B-85

; Sequence 85, Application US/10467962B

; Publication No. US20050246784A1

; GENERAL INFORMATION:

; APPLICANT: Plesch, Gunnar

; APPLICANT: Blau, Astrid

; APPLICANT: Daeschner, Klaus

; APPLICANT: Klein, Mathieu

; TITLE OF INVENTION: Identification of Herbicidally Active Substances

; FILE REFERENCE: 2000 857

; CURRENT APPLICATION NUMBER: US/10/467,962B

; CURRENT FILING DATE: 2003-08-14

; PRIOR APPLICATION NUMBER: PCT/EP02/01466

; PRIOR FILING DATE: 2002-02-13

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn Vers. 2.0

; SEQ ID NO 85

; LENGTH: 423

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-467-962B-85

Query Match

Best Local Similarity 75.9%; Score 22; DB 1; Length 423;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRAPVI 6

Db 270 MRIPVL 275

RESULT 8

US-10-967-648A-2

; Sequence 2, Application US/10967648A

; Publication No. US20050245473A1

; GENERAL INFORMATION:

; APPLICANT: Saunders, Nicholas A

; TITLE OF INVENTION: Differentiation- and/or proliferation-modulating agents and uses

; FILE REFERENCE: 12493972

; CURRENT APPLICATION NUMBER: US/10/967,648A

; CURRENT FILING DATE: 2004-10-15

; PRIOR APPLICATION NUMBER: USSN 60/512010

; PRIOR FILING DATE: 2003-10-16

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 437

; TYPE: PRT

; ORGANISM: Human

US-10-967-648A-2

Query Match

Best Local Similarity 75.9%; Score 22; DB 1; Length 437;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5

Db 365 LRAPV 369

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RESULT 9
US-11-034-569-16
; Sequence 16, Application US/11034569
; Publication No. US20050251876A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company
; TITLE OF INVENTION: Aspartate Kinase
; FILE REFERENCE: B1430 PCT
; CURRENT APPLICATION NUMBER: US/11/034,569
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: US/09/890,813
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: PCT/US00/34396
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172944
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-034-569-16

Query Match 75.9%; Score 22; DB 7; Length 439;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAPVI 6
Db 425 RAPVL 429

RESULT 10
US-11-022-562-211
; Sequence 211, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 2280
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-11-022-562-211

Query Match 75.9%; Score 22; DB 7; Length 2280;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
Db 1205 MRSPV 1209

RESULT 11
US-11-016-706-10
; Sequence 10, Application US/11016706
; Publication No. US2005024334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-706-10

Query Match 72.4%; Score 21; DB 7; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
Db 7 IRAPV 11

RESULT 12
US-10-986-501-357
; Sequence 357, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 357
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-357

Query Match 72.4%; Score 21; DB 1; Length 78;
Best Local Similarity 80.0%; Pred. No. 7.8;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRAPV 5
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Db 58 IRAPV 62

RESULT 13

US-10-982-545-4
; Sequence 4, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cystatin C precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(26)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (27)..(146)
; OTHER INFORMATION: Biomarker peptide M13391, full-length Cystatin C
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (35)..(146)
; OTHER INFORMATION: Biomarker peptide M12583.4, truncated Cystatin C
; US-10-982-545-4

Query Match 72.4%; Score 21; DB 1; Length 146;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
:|||||
Db 5 LRAPL 10

RESULT 14

US-11-016-706-38
; Sequence 38, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO

; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 38
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-706-38

Query Match 72.4%; Score 21; DB 7; Length 416;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5
:|||||
Db 356 IRAPV 360

RESULT 15

US-10-636-716-2
; Sequence 2, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-10-636-716-2

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
|||
Db 1 MRAP 4

RESULT 16
US-10-636-716-14
; Sequence 14, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Choon J.
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-10-636-716-14

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
|||
Db 1 MRAP 4

RESULT 17
US-10-636-716-16
; Sequence 16, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Choon J.
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-16

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
|||
Db 1 MRAP 4


```
RESULT 18
US-10-636-716-18
; Sequence 18, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-18
Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 19
US-10-636-716-20
; Sequence 20, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-18
Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 20
US-10-636-716-22
; Sequence 22, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-20
Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4
```

```
/
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
US-10-636-716-22

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 21
US-10-636-716-24
; Sequence 24, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
```

```
/
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
US-10-636-716-24

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 22
US-10-636-716-26
; Sequence 26, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
```

REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-10-636-716-26

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
DB 1 MRAP 4

RESULT 23
US-10-636-716-28
; Sequence 28, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-10-636-716-28

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
DB 1 MRAP 4

RESULT 24
US-10-636-716-30
; Sequence 30, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-30

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
|||
Db 1 MRAP 4

RESULT 25

US-10-636-716-32
; Sequence 32, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-32

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
|||
Db 1 MRAP 4

RESULT 26

US-10-636-716-34
; Sequence 34, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:

; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-10-636-716-34

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
|||
Db 1 MRAP 4

RESULT 27

US-10-636-716-36
; Sequence 36, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-10-636-716-36

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
DB 1 MRAP 4

RESULT 28
US-10-636-716-38
Sequence 38, Application US/10636716
Publication No. US20050244832A9
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-10-636-716-38

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
DB 1 MRAP 4

RESULT 29
US-10-636-716-40
Sequence 40, Application US/10636716
Publication No. US20050244832A9
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305

```
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-10-636-716-40

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
Db 1 MRAP 4

RESULT 30
US-10-636-716-42
/ Sequence 42, Application US/10636716
/ Publication No. US20050244832A9
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Kho, Choon J.
/ APPLICANT: Jelmsberg, Anna C.
/ APPLICANT: Adams, Robyn L.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Farrah, Theresa M.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-10-636-716-44
```

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-10-636-716-42

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
Db 1 MRAP 4

RESULT 31
US-10-636-716-44
/ Sequence 44, Application US/10636716
/ Publication No. US20050244832A9
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Kho, Choon J.
/ APPLICANT: Jelmsberg, Anna C.
/ APPLICANT: Adams, Robyn L.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Farrah, Theresa M.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/636,716
/ FILING DATE: 07-AUG-2003
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,087
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/803,305
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-24C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 553 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ US-10-636-716-44

Query Match 72.4%; Score 21; DB 1; Length 553;
```

```
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 32
US-10-636-716-46
; Sequence 46, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-46

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 33
US-10-636-716-48
; Sequence 48, Application US/10636716
; Publication No. US20050244832A9
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-10-636-716-48

Query Match 72.4%; Score 21; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAP 4
Db 1 MRAP 4

RESULT 34
US-11-109-156-23
; Sequence 23, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
```

/ APPLICANT: Tomoyasu Sugiyama
/ APPLICANT: Ai Wakamatsu
/ APPLICANT: Keiichi Nagai
/ APPLICANT: Tetsuji Otsuki
/ APPLICANT: Shin-ichi Funahashi
/ APPLICANT: Chiaki Senoo
/ APPLICANT: Jun-ichi Nezu
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
/ TITLE OF INVENTION: PHOSPHATASE
/ FILE REFERENCE: 06501-099002
/ CURRENT APPLICATION NUMBER: US/11/109,156
/ CURRENT FILING DATE: 2005-04-19
/ PRIOR APPLICATION NUMBER: US/10/060,065
/ PRIOR FILING DATE: 2003-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP00/05061
/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/159,590
/ PRIOR FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US 60/183,322
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: JP 11-248036
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: JP 2000-118776
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: JP 2000-183767
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: JP 2000-241899
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 23
/ LENGTH: 1338
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-109-156-23

Query Match 72.4%; Score 21; DB 7; Length 1338;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAP 4
DB 1119 MRAP 1122

RESULT 35
US-10-510-386-82
/ Sequence 82, Application US/10510386
/ Publication No. US2005024922A1
/ GENERAL INFORMATION:
/ APPLICANT: Andersen, Jens Tonne
/ APPLICANT: Clausen, Ib Groth
/ APPLICANT: Jorgensen, Steen Troels
/ APPLICANT: Olsen, Peter Bjarke
/ APPLICANT: Rasmussen, Michael Dolberg
/ TITLE OF INVENTION: Improved Bacillus Host Cell
/ FILE REFERENCE: 10294.204-US
/ CURRENT APPLICATION NUMBER: US/10/510,386
/ CURRENT FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 248
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 82
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Bacillus licheniformis
US-10-510-386-82

Query Match 69.0%; Score 20; DB 1; Length 330;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 1119 MRAP 1122

DB 272 MRAPVI 277
RESULT 36
US-10-981-873-28
/ Sequence 28, Application US/10981873
/ Publication No. US20050250680A1
/ GENERAL INFORMATION:
/ APPLICANT: Walensky, Loren D.
/ APPLICANT: Koremeyer, Stanley J.
/ APPLICANT: Verdine, Gregory
/ TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: 00530-124001
/ CURRENT APPLICATION NUMBER: US/10/981,873
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US 60/517,848
/ PRIOR FILING DATE: 2003-11-05
/ PRIOR APPLICATION NUMBER: US 60/591,548
/ PRIOR FILING DATE: 2004-07-27
/ NUMBER OF SEQ ID NOS: 117
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-981-873-28

Query Match 69.0%; Score 20; DB 1; Length 352;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 142 IRAPML 147

RESULT 37
US-10-131-826A-334
/ Sequence 334, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117

;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059122
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059184
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 334
;; LENGTH: 433
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-131-826A-334

Query Match 69.0%; Score 20; DB 1; Length 433;
Best Local Similarity 80.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 222 QAPVI 226

RESULT 38
US-11-074-176-312
; Sequence 312, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-312

Query Match 69.0%; Score 20; DB 7; Length 435;
Best Local Similarity 80.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 348 KAPV 352

RESULT 39
US-11-074-176-50
; Sequence 50, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

;; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
;; FILE REFERENCE: 5051-694
;; CURRENT APPLICATION NUMBER: US/11/074,176
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: 60/551,161
;; PRIOR FILING DATE: 2004-03-08
;; NUMBER OF SEQ ID NOS: 381
;; SOFTWARE: FastSEQ for Windows Version 4.0
;; SEQ ID NO 50
;; LENGTH: 456
;; TYPE: PRT
;; ORGANISM: Lactobacillus acidophilus
US-11-074-176-50

Query Match 69.0%; Score 20; DB 7; Length 456;
Best Local Similarity 80.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 369 KAPV 373

RESULT 40
US-10-336-263A-8
; Sequence 8, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACT
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336,263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Nostoc punctiforme
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(480)
; OTHER INFORMATION:
US-10-336-263A-8

Query Match 69.0%; Score 20; DB 1; Length 480;
Best Local Similarity 80.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAPVI 6
Db 346 RTEVI 350

Search completed: November 18, 2005, 21:40:16
Job time : 2.71429 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 18, 2005, 20:58:55 ; Search time 12.4286 seconds
(without alignments)
46.449 Million cell updates/sec

Title: US-10-029-926D-8
Perfect score: 29
Sequence: 1 MRAPVI 6
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	249	2 H87675	hydrolase, alpha/b
2	29	100.0	442	2 JC4733	probable H+-transp
3	29	100.0	629	2 T37255	acetylcholinestera
4	28	96.6	425	2 S33045	hypothetical prote
5	27	93.1	247	2 H69030	coenzyme PQ synth
6	26	89.7	286	2 A91131	tagatose-1,6-bisph
7	26	89.7	286	2 A85976	tagatose-bisphosph
8	26	89.7	286	2 E65103	tagatose-bisphosph
9	26	89.7	327	2 E72057	ferrochelatase [im
10	26	89.7	327	2 H86565	ferrochelatase [im
11	26	89.7	450	1 S13730	pmbA protein - Esc
12	26	89.7	450	2 AE1056	probable PmbA prot
13	26	89.7	450	2 D86121	maturation of anti
14	26	89.7	450	2 D91280	maturation of anti
15	25	86.2	138	2 T2416	hypothetical prote
16	25	86.2	147	2 C95907	probable protein i
17	25	86.2	147	2 F95924	hypothetical prote
18	25	86.2	149	2 C72419	conserved hypotet
19	25	86.2	154	2 A82812	conserved hypotet
20	25	86.2	163	2 A87412	hypothetical prote
21	25	86.2	195	2 F75399	antibiotic resista
22	25	86.2	196	2 G75405	probable amidotran
23	25	86.2	203	2 C84409	imidazoleglycerol-
24	25	86.2	222	2 S63320	probable membrane
25	25	86.2	222	2 S56195	probable membrane
26	25	86.2	224	2 S55081	hypothetical prote
27	25	86.2	227	2 C53304	transfer protein C
28	25	86.2	240	2 E69004	hypothetical prote
29	25	86.2	252	2 A88508	protein H14A12.4 [

hisF protein limpo
tryptophan synthas
fructose-1,6-bipho
fructose-1,6-bipho
conserved hypotet
glyceraldehyde 3-p
fructose-bisphosph
hypothetical prote
hypothetical prote
lipoprotein releas
probable two-compo
hypothetical prote
pmbA protein limpo
L-seryl-tRNAse se
hypothetical prote
shaw protein - Cal
probable sugar kin
inositol-3-phospha
glycoprotein E - h
ABC transporter, A
hypothetical prote
hypothetical prote
cytochrome C-type
hypothetical prote
translation initia
gag polyprotein -
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
T-cell receptor ga
ribosomal protein
hypothetical prote
hypothetical prote
CBS domain-contain
hypothetical prote
alkB protein - Esc
AlkB protein limpo
alkylated DNA repa
DNA repair system
arginine ABC trans
fructose-bisphosph
galactosyltransfer
triophosphate is
hypothetical prote
amphiregulin precu
triophosphate is
translation initia
probable dehydroge
hypothetical prote
O-antigen export s
dolichol-phosphate
dolichol-phosphate
ferredoxin-type pr
ferredoxin-type pr
ferredoxin-type pr
ferredoxin-type pr
l-rhamnose operon
hypothetical prote
hypothetical prote
sopB protein - Esc
hypothetical prote
hypothetical cyste
fructose-bisphosph
fructose-bisphosph
protein w10g11.7 [
DNA-methyltransfer
general secretion
probable CDP-tyrel

ALIGNMENTS

RESULT 1
H87675
hydrolase, alpha/beta hydrolase fold family [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 12-Jul-2004
C/Accession: H87675
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: H87675
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <STO>
A/Cross-references: UNIPROT:Q9A2W4; UNIPARC:UPI00000C7A9C; GB:AE005673; NID:G13425158; E
C/Genetics:
A/Gene: CC3442
C/Superfamily: tropinesterase

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
DB 1 MRAPVI 6

RESULT 2
JC4733
probable H+-transporting two-sector ATPase (EC 3.6.3.14), flagellum-specific - Rhodobact
C/Species: Rhodobacter sphaeroides
C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 31-Dec-2004
C/Accession: JC4733
R.Ballado, T.; Campos, A.; Camarena, L.; Dreyfus, G.
Gene 170, 69-72, 1996
A/Title: Flagellar genes from Rhodobacter sphaeroides are homologous to genes of the fl
A/Reference number: JC4733; MUID:96200857; PMID:8621091
A/Accession: JC4733
A/Molecule type: DNA
A/Residues: 1-442 <BAL>
A/Cross-references: UNIPROT:Q53093; UNIPARC:UPI00000A0E610; GB:U31090; NID:G1518877; PIDN
C/Genetics:
A/Gene: fliI
C/Superfamily: H(+)-transporting ATP synthase; H+-transporting ATP synthase alpha chain
C/Keywords: ATP; flagellum; hydrolase; nucleotide binding; P-loop
F.168-175/Region: nucleotide-binding motif A (P-loop)
F.191-362/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
F.191-207/Region: ATP-binding #status predicted
F.242-258/Domain: beta chain #status predicted <BET>

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
DB 77 MRAPVI 82

RESULT 3
T37255
acetylcholinesterase (EC 3.1.1.7) 2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37255
R.Grauso, M.; Culetto, E.; Combes, D.; Fedon, Y.; Toutant, J.P.; Arpagaus, M.
FEBS Lett. 424, 279-284, 1998

Query Match 93.1%; Score 27; DB 2; Length 247;

A/Title: Existence of four acetylcholinesterase genes in the nematodes Caenorhabditis el
A/Reference number: Z21648; MUID:98198570; PMID:9539167
A/Accession: T37255
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-629 <GRA>
A/Cross-references: UNIPROT:O61371; UNIPARC:UPI000007D0A5; EMBL:AF025378; NID:G5148937;
A/Experimental source: strain N2
C/Genetics:
A/Gene: ace-2
A/Map position: I
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase

Query Match 100.0%; Score 29; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
DB 1 MRAPVI 6

RESULT 4
S33045
hypothetical protein - human herpesvirus 4
C/Species: human herpesvirus 4, Epstein-Barr virus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33045
R.Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A/Reference number: S32973
A/Accession: S33045
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-425 <FAR>
A/Cross-references: UNIPROT:P30119; UNIPARC:UPI000000CDF1; EMBL:V01555; NID:G59074; PIDN
C/Superfamily: equine herpesvirus 2 hypothetical protein 23

Query Match 96.6%; Score 28; DB 2; Length 425;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
|||||
DB 87 MRAPVI 92

RESULT 5
H69030
coenzyme PQQ synthetase protein III - Methanobacterium thermoautotrophicum (strain Delta
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: H69030
R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: H69030
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-247 <MTH>
A/Cross-references: UNIPROT:O27295; UNIPARC:UPI0000006654F; GB:AE000890; GB:AE000666; NID
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1227
A/Start codon: GTG
C/Keywords: iron; metalloprotein
F.34,38,41/Binding site: iron (Cys) #status predicted

Query Match 93.1%; Score 27; DB 2; Length 247;

Best Local Similarity 66.7%; Pred. No. 43;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 4 MRAPIV 9

RESULT 6
tagatose-1,6-bisphosphate aldolase [imported] - Escherichia coli (strain O157:H7, substra
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A91131
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A95629; MUID:21156231; PMID:11258796
A:Accession: A91131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HAY>
A:Cross-references: UNIPROT:P42908; UNIPARC:UPI0000111A15; GB:BA000007; PIDN:BA037440.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs4017
C:Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 41 MRSPVI 46

RESULT 7
tagatose-bisphosphate aldolase 2 [imported] - Escherichia coli (strain O157:H7, substra
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85976
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <STO>
A:Cross-references: UNIPROT:P42908; UNIPARC:UPI0000111A15; GB:AE005174; NID:g12517735; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: agay
C:Superfamily: fructose-bisphosphate aldolase II

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 41 MRSPVI 46

RESULT 8
tagatose-bisphosphate aldolase agay (BC 4.1.2.-) - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C:Accession: E65103
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65103
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <BLAT>
A:Cross-references: UNIPROT:P42908; UNIPARC:UPI0000111A15; GB:AE000395; GB:U000096; NID:
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: agay
C:Superfamily: fructose-bisphosphate aldolase II
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 89.7%; Score 26; DB 2; Length 286;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 41 MRSPVI 46

RESULT 9
E72057
ferrochelatase CP0144 [imported] - Chlamydomophila pneumoniae (strains CWL029 and AR39)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: E72057; F81609
R:Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <ARN>
A:Cross-references: UNIPROT:Q927V1; UNIPARC:UPI000012C5CF; GB:AE001645; GB:AE001363; N
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBby, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81609
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <REA>
A:Cross-references: UNIPARC:UPI000012C5CF; GB:AE002175; GB:AE002161; NID:g7189069; PIDN
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: hemZ; CP0144
C:Superfamily: ferrochelatase

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 86 LRAPVI 91

RESULT 10
H86565
ferrochelatase [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86565
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I

Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: H86565
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <STO>
A:Cross-references: UNIPROT:Q9ZTV1; UNIPARC:UPI00001656B0; GB:BA000008; NID:g8978975; PMID:10871362
A:Experimental source: strain J138
C:Genetics:
A:Gene: hemZ

Query Match 89.7%; Score 26; DB 2; Length 327;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 86 LRAPVI 91

RESULT 11
S13730
pmbA protein - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 29-Jan-1999 #sequence revision 29-Jan-1999 #text_change 09-Jul-2004
A:Accession: S13730; S56461; F65235
R:Rodriguez-Sainz, M.C.; Hernandez-Chico, C.; Moreno, F.
Mol. Microbiol. 4, 1921-1932, 1990
A>Title: Molecular characterization of pmbA, an Escherichia coli chromosomal gene required for pili assembly
A:Reference number: S13730; MUID:91186828; PMID:2082149
A:Accession: S13730
A:Molecule type: DNA
A:Residues: 1-450 <RO>
A:Cross-references: UNIPROT:P24231; UNIPARC:UPI0000131CAF; EMBL:X54152; NID:g42439; PMID:2082149
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A>Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.1 to 92.9 Mb
A:Reference number: S56314; MUID:95334362; PMID:7610040
A:Accession: S56461
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-450 <BUR>
A:Cross-references: UNIPARC:UPI0000131CAF; EMBL:U14003; NID:gl263172; PIDN:AAA97132.1; F65235
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-450 <BLAT>
A:Cross-references: UNIPARC:UPI0000131CAF; GB:AE000494; GB:U00096; NID:gl790670; PIDN:AA000001
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: pmbA
A:Map position: 96 min
C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 1; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 242 MKAPVI 247

RESULT 12
AE1056
probable PmbA protein pmbA [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
A:Accession: AE1056
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Paratyphi C
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE1056
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <PAR>
A:Cross-references: UNIPARC:UPI000005A965; GB:AL513382; PIDN:CAD006898.1; PID:gl6505546; C:Genetics:
A:Gene: pmbA
C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 242 MKAPVI 247

RESULT 13
D86121
maturation of antibiotic MccB17, see tld genes [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A:Accession: D86121
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D86121
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <STO>
A:Cross-references: UNIPROT:P24231; UNIPARC:UPI0000131CAF; GB:AE005174; NID:gi2519236; C:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: pmbA
C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 242 MKAPVI 247

RESULT 14
D91280
maturation of antibiotic MccB17 [imported] - Escherichia coli (strain O157:H7, substrain O157:H7)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A:Accession: D91280
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D91280
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-450 <HAY>
A:Cross-references: UNIPROT:P24231; UNIPARC:UPI0000131CAF; GB:BA000007; PIDN:BA83635.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs5212
C:Superfamily: Escherichia coli pmbA protein

Query Match 89.7%; Score 26; DB 2; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 6
|:|||||
Db 242 MRAPV 247

RESULT 15
T24916
hypothetical protein T14G10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24916
R:Wild, A.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19954
A:Accession: T24916
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-138 <WIL>
A:Cross-references: UNIPROT:Q22499; UNIPARC:UPI000007C3C7; EMBL:Z68880; PIDN:CRA93096.1;
A:Experimental source: clone T14G10
C:Genetics:
A:Gene: CESP:T14G10.4
A:Map position: 4
A:Introns: 52/3; 108/2

Query Match 86.2%; Score 25; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5
|:|||||
Db 1 MRAPV 5

RESULT 16
C95907
probable protein in ISRM14 [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95907
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95907
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <KUR>
A:Cross-references: UNIPROT:Q92W24; UNIPARC:UPI00000CB5F6; GB:AL591985; PIDN:CAC48923.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20543
A:Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5
|:|||||
Db 143 MRAPV 147

RESULT 17
F95924
hypothetical protein Smb21083 [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95924
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: F95924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <KUR>
A:Cross-references: UNIPROT:Q92VN7; UNIPARC:UPI00000CB5F6; GB:AL591985; PIDN:CAC49062.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb21083
A:Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPV 5
|:|||||
Db 143 MRAPV 147

RESULT 18
C72419
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72419
R:Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <ARN>
A:Cross-references: UNIPROT:Q9WY76; UNIPARC:UPI00000C148A; GB:AE001695; PIDN:AE000512; NI
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TW0081

Query Match 86.2%; Score 25; DB 2; Length 149;
Best Local Similarity 66.7%; Pred. No. 81; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 109 LRAPVI 114

RESULT 19

A82812
conserved hypothetical protein XF0404 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: A82812
R/Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: A82812
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-154 <STM>
A/Cross-references: UNIPROT:Q9PG98; UNIPARC:UPI00000C23D1; GB:AE003891; GB:AE003849; NID
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurama, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A/Authors: Martins, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XP0404

Query Match 86.2%; Score 25; DB 2; Length 154;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 75 VRAPVI 80

RESULT 20

A87412
hypothetical protein CC1312 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: A87412
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: A87412
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-163 <STO>
A/Cross-references: UNIPROT:Q9A8P1; UNIPARC:UPI00000C7341; GB:AE005673; NID:gl3422653; F
C/Genetics:
A/Gene: CC1312

Query Match 86.2%; Score 25; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5

Db 1 MRAPV 5
:|||||

RESULT 21

F75399
antibiotic resistance protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: F75399
R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: F75399
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-195 <WHI>
A/Cross-references: UNIPROT:Q9RUG7; UNIPARC:UPI00000D3E53; GB:AE001986; GB:AE000513; NID
A/Experimental source: strain R1
C/Genetics:
A/Gene: DRI419
A/Map position: 1
C/Superfamily: tunicamycin resistance protein

Query Match 86.2%; Score 25; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 4 MRSPV 9

RESULT 22

G75405
probable amidotransferase Hish - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: G75405
R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: G75405
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-196 <WHI>
A/Cross-references: UNIPROT:Q9RUL8; UNIPARC:UPI00000D3E3B; GB:AE001982; GB:AE000513; NID
A/Experimental source: strain R1
C/Genetics:
A/Gene: DRI366
A/Map position: 1
C/Superfamily: conserved hypothetical protein H11648

Query Match 86.2%; Score 25; DB 2; Length 196;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 138 IRAPVI 143

RESULT 23

C84409
imidazoleglycerol-phosphate synthase [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84409
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: C84409
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-203 <STO>
 A:Cross-references: UNIPROT:Q9HMD2; UNIPARC:UPI0000063B98; GB:AE004437; NID:g10581980; F
 C:Genetics:
 A:Gene: hishi
 C:Superfamily: conserved hypothetical protein H11648

Query Match 86.2%; Score 25; DB 2; Length 203;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 Db 141 IRAPVI 146

RESULT 24
 S63320
 probable membrane protein YNL334c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein N0285
 C:Species: Saccharomyces cerevisiae
 C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C:Accession: S63320
 R:Obermaier, B.; Piravandi, E.; Rinke, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63317
 A:Accession: S63320
 A:Molecule type: DNA
 A:Residues: 1-222 <OBE>
 A:Cross-references: UNIPROT:P53823; UNIPARC:UPI000013BAA0; EMBL:Z71610; NID:g1302458; PI
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:SNO2
 A:Cross-references: SGD:S0005278; MIPS:YNL334C
 A:Map position: 14L
 C:Superfamily: conserved hypothetical protein H11648
 C:Keywords: transmembrane protein
 F,2-18/Domain: transmembrane #status predicted <TMM>

Query Match 86.2%; Score 25; DB 2; Length 222;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 Db 151 IRAPVI 156

RESULT 25
 S56195
 probable membrane protein YFL060c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein R005
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C:Accession: S56195; S62277
 R:Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu
 submitted to the EMBL Data Library, May 1995
 A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
 A:Reference number: S56186
 A:Accession: S56195
 A:Molecule type: DNA
 A:Residues: 1-222 <MUR>
 A:Cross-references: UNIPROT:P43544; UNIPARC:UPI000013AE6E; EMBL:D50617; NID:g836685; PID

R:Murakami, Y.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S62230
 A:Accession: S62277
 A:Molecule type: DNA
 A:Residues: 92-222 <MUW>
 A:Cross-references: UNIPARC:UPI0000178AD0; EMBL:D44603; NID:g871957; PID:g871966
 C:Genetics:
 A:Gene: SGD:SNO3
 A:Cross-references: SGD:S0001834; MIPS:YFL060c
 A:Map position: 6L
 C:Superfamily: conserved hypothetical protein H11648
 C:Keywords: transmembrane protein
 F,2-18/Domain: transmembrane #status predicted <TMM>

Query Match 86.2%; Score 25; DB 2; Length 222;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 Db 151 IRAPVI 156

RESULT 26
 S55081
 hypothetical protein YMR095c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YM6543.02c
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S55081
 R:Hunt, S.; Bowman, S.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S55080
 A:Accession: S55081
 A:Molecule type: DNA
 A:Residues: 1-224 <HUN>
 A:Cross-references: UNIPROT:Q03144; UNIPARC:UPI000013BA47; EMBL:Z49807; NID:g854430; PI
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD:SNO1
 A:Cross-references: SGD:S0004701; MIPS:YMR095c
 A:Map position: 13R
 C:Superfamily: conserved hypothetical protein H11648

Query Match 86.2%; Score 25; DB 2; Length 224;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 Db 160 IRAPVI 165

RESULT 27
 C53304
 transfer protein C - plasmid R64
 C:Species: plasmid R64
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jul-2000
 C:Accession: C53304
 R:Kim, S.R.; Funayama, N.; Komano, T.
 J. Bacteriol. 175, 5035-5042, 1993
 A:Title: Nucleotide sequence and characterization of the traABCD region of IncII plasmid
 A:Reference number: A53304; MUID:93352408; PMID:8349545
 A:Accession: C53304
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-227 <KIM>
 A:Cross-references: UNIPARC:UPI000008BA04; GB:D88588; GB:D14607; NID:g4903079; PID:BAA
 C:Genetics:
 A:Gene: trac
 A:Genome: plasmid
 C:Superfamily: plasmid R64 transfer protein C

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Query Match      86.2%; Score 25; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
    |||||
Db 149 MRAPV 153

RESULT 28
E69004
hypothetical protein MTH1030 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69004
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwni, N.
; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func0
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69004
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Map position: not shown
A:Molecule type: DNA
A:Residues: 1-240 <MTH>
A:Cross-references: UNIPROT:Q27109; UNIPARC:UPI0000062C45; GB:AE000875; GB:AE000666; NID
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1030

Query Match      86.2%; Score 25; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 6
    |||||
Db 37 VRAPV 42

RESULT 29
A88508
protein H14A12.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A88508
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: A88508
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-252 <STO>
A:Cross-references: UNIPROT:O17212; UNIPARC:UPI0000080D4C; GB:chr_III; PIDN:AAB70985.1;
A:Note: strong similarity to Brachyury-like proteins
C:Genetics:
A:Gene: H14A12.4
A:Map position: 3

Query Match      86.2%; Score 25; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
    |||||
Db 128 MRAPV 132

RESULT 30
AC3507

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hisF protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3507
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3507
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <KUR>
A:Cross-references: UNIPROT:Q8YE37; UNIPARC:UPI00000582DC; GB:AE008917; PIDN:AAL53222.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI2041
A:Map position: 1
C:Superfamily: cyclase hisF

Query Match      86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 6
    |||||
Db 200 VRAPV 205

RESULT 31
AC2407
tryptophan synthase alpha chain [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2407
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriatz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2407
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <KUR>
A:Cross-references: UNIPROT:Q8YVM3; UNIPARC:UPI000000C6C69; GB:BA000019; PIDN:BA076510.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: trpA
C:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology

Query Match      86.2%; Score 25; DB 2; Length 266;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 6
    |||||
Db 92 LRAPV 97

RESULT 32
AF1341
fructose-1,6-bisphosphate aldolase type II homolog lmo2134 [imported] - Listeria monocytoc
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1341
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Faihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.

```

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1341

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-284 <GLA>

A:Cross-references: UNIPROT:Q8Y5D1; UNIPARC:UPI000005574E; GB:NC_003210; PIDN:CAD00212.1

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: imo2134

C:Superfamily: fructose-bisphosphate aldolase II

Query Match 86.2%; Score 25; DB 2; Length 284;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

:|||:

Db 40 LRAPII 45

RESULT 33

AD1712

fructose-1,6-bisphosphate aldolase type II homolog lin2239 [imported] - *Listeria innocua*

C:Species: *Listeria innocua*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1712

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,

A:Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1712

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-284 <GLA>

A:Cross-references: UNIPROT:Q929N5; UNIPARC:UPI000000C07CF; GB:AL592022; PIDN:CAC97468.1;

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: lin2239

C:Superfamily: fructose-bisphosphate aldolase II

Query Match 86.2%; Score 25; DB 2; Length 284;

Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

:|||:

Db 40 LRAPII 45

RESULT 34

G96024

conserved hypothetical exported protein SMB20771 [imported] - *Sinorhizobium meliloti* (se

C:Species: *Sinorhizobium meliloti*

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: G96024

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmaster, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: G96024

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-328 <KUR>

A:Cross-references: UNIPROT:Q92TP4; UNIPARC:UPI000000CB88F; GB:AL591985; PIDN:CAC49863.1;

A:Experimental source: strain 1021, megaplasmid pSymB

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, h
ebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMB20771

A:Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 328;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6

:|||:

Db 59 MKAPV 64

RESULT 35

C81285

glyceraldehyde 3-phosphate dehydrogenase Cj1403c [imported] - *Campylobacter jejuni* (str.

C:Species: *Campylobacter jejuni*

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: C81285

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre

Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals h

A:Reference number: AB1250; MUID:20150912; PMID:10688204

A:Accession: C81285

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-332 <PAR>

A:Cross-references: UNIPROT:Q9PMQ4; UNIPARC:UPI000000C1EF9; GB:AL139078; GB:AL111168; NT

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: gapA; Cj1403c

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 86.2%; Score 25; DB 2; Length 332;

Best Local Similarity 83.3%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPVI 6

:|||:

Db 230 MRVPVI 235

RESULT 36

AI0112

fructose-bisphosphate aldolase (EC 4.1.2.13) [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AI0112

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0112

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-359 <KUR>

A:Cross-references: UNIPROT:Q8ZHH4; UNIPARC:UPI000000DCE0D; GB:AL590842; PIDN:CAC89764.1

C:Genetics:

A:Gene: fbaA

C:Superfamily: fructose-bisphosphate aldolase II

C:Keywords: aldehyde-lyase, carbon-carbon lyase

Query Match 86.2%; Score 25; DB 2; Length 359;

Best Local Similarity 83.3%; Pred. No. 2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 53 VRAPVI 58

RESULT 37

F90200
hypothetical protein SS00543 [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: F90200
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayer, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: F90200
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-362 <KUR>
A/Cross-references: UNIPROT:Q9UWU8; UNIPARC:UPI0000064A2C; GB:AE006641; NID:gl13813705; F
C/Genetics:
A/Gene: SS00543

Query Match 86.2%; Score 25; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 288 LRAPV 293

RESULT 38

B70752
hypothetical protein Rv0106 - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C/Accession: B70752
R/Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
i Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: B70752
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-398 <COL>
A/Cross-references: UNIPROT:Q10899; UNIPARC:UPI000013928E; GB:Z74410; GB:AL123456; NID:G
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: Rv0106
C/Supfamily: conserved hypothetical protein yciC

Query Match 86.2%; Score 25; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
:|||||
Db 1 MRTPVI 6

RESULT 39

AB3394
lipoprotein releasing system transmembrane protein lolo [imported] - Brucella melitensis
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: AB3394

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessa,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A/Reference number: AD3252; PMID:11756688
A/Accession: AE3394
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-422 <KUR>
A/Cross-references: UNIPROT:Q8YGL9; UNIPARC:UPI0000057F5C; GB:AE008917; PIDN:AA152320.1;
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME11139
A/Map position: 1
C/Supfamily: hypothetical protein H11555

Query Match 86.2%; Score 25; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
:|||||
Db 245 MRAPV 249

RESULT 40

E83083
probable two-component sensor PA4494 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: E83083
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: E83083
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-422 <STO>
A/Cross-references: UNIPROT:Q9HV57; UNIPARC:UPI000000C5D36; GB:AE004863; GB:AE004091; NID
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA4494

Query Match 86.2%; Score 25; DB 2; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPV 5
:|||||
Db 1 MRAPV 5

Search completed: November 18, 2005, 21:15:20
Job time : 17.4286 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:58:05 ; Search time 77.7857 Seconds
(without alignments)
54.421 Million cell updates/sec

Title: US-10-029-926D-8

Perfect score: 29

Sequence: 1 MRAPV1 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	249	Q9A2M4 CAUCR	Q9A2M4 caulobacter
2	29	100.0	309	Q63ZV1 MOUSE	Q63ZV1 mus musculus
3	29	100.0	442	Q53093 RHOSH	Q53093 rhodobacter
4	29	100.0	442	Q53153 RHOSH	Q53153 rhodobacter
5	29	100.0	629	Q61371 CAEEL	Q61371 caenorhabditis
6	29	100.0	939	Q6PD31 MOUSE	Q6PD31 mus musculus
7	29	100.0	947	Q80TL6 MOUSE	Q80TL6 mus musculus
8	28	96.6	164	RHBD1_RAT	RHBD1_RAT
9	28	96.6	212	Q5TKT1 BRARE	Q5TKT1 brachydanio
10	28	96.6	231	Q6PD44 ACTAD	Q6PD44 acinetobacter
11	28	96.6	359	Q4NFV3 9MICC	Q4NFV3 arthrobacter
12	28	96.6	373	RHBD1_MOUSE	RHBD1_MOUSE
13	28	96.6	376	Q4UEE2 XANCP	Q4UEE2 xanthomonas
14	28	96.6	376	Q8P9F5 XANCP	Q8P9F5 xanthomonas
15	28	96.6	425	YTRI_EBV	YTRI_EBV
16	28	96.6	425	Q777C1 9GAMA	Q777C1 human herpes
17	28	96.6	438	RHBD1_HUMAN	RHBD1_HUMAN
18	28	96.6	486	Q5CWF0 CRYPV	Q5CWF0 cryptospori
19	28	96.6	486	Q5CG10 CRYHO	Q5CG10 cryptospori
20	28	96.6	520	Q4S4R8 TETNG	Q4S4R8 tetraodon n
21	28	96.6	541	Q8NT69 CORGL	Q8NT69 corynebacte
22	28	96.6	577	Q6CYG6 KLULA	Q6CYG6 kluyveromyce
23	28	96.6	713	Q7YVY3 CRYPV	Q7YVY3 cryptospori
24	27	93.1	152	Q4I8P3 GIBZE	Q4I8P3 gibberella
25	27	93.1	179	Q5ESV3 VIBF1	Q5ESV3 vibrio fisc
26	27	93.1	198	Q51VA7 MAGGR	Q51VA7 magnaporthe
27	27	93.1	247	Q27295 METTH	Q27295 methanobact
28	27	93.1	333	Q5GZK0 XANOR	Q5GZK0 xanthomonas
29	27	93.1	376	Q9L778 XANOR	Q9L778 xanthomonas
30	27	93.1	376	Q8PL69 XANAC	Q8PL69 xanthomonas
31	27	93.1	416	Q9ACQ9_STRCO	Q9ACQ9 streptomyce

32	27	93.1	436	2	Q4FPU9 9GAMM	Q4FPU9 psychrobact
33	27	93.1	449	2	Q89X81 BRAJA	Q89X81 brachydanio
34	27	93.1	535	1	TLE1 BRARE	TLE1 brachydanio
35	27	93.1	771	2	Q98TH2 BRARE	Q98TH2 brachydanio
36	26	89.7	135	2	Q4JBH8 SULAC	Q4JBH8 sulfolobus
37	26	89.7	162	2	Q8ILB7 PLAF7	Q8ILB7 plasmodium
38	26	89.7	162	2	Q7RLI3 PLACH	Q7RLI3 plasmodium
39	26	89.7	162	2	Q4XEB4 PLACH	Q4XEB4 plasmodium
40	26	89.7	162	2	Q4VVT2 PLABE	Q4VVT2 plasmodium
41	26	89.7	199	2	Q6BSE3 DEBHA	Q6BSE3 debaromyce
42	26	89.7	214	2	Q5KW43 GROKA	Q5KW43 geobacillus
43	26	89.7	219	2	Q4FS71 9GAMM	Q4FS71 psychrobact
44	26	89.7	226	2	Q5AIY2 CANAL	Q5AIY2 candida alb
45	26	89.7	226	2	Q5AI51 CANAL	Q5AI51 candida alb
46	26	89.7	250	1	PDXJ BRAJA	Q69158 brachydanio
47	26	89.7	264	2	Q7F2A7 ORYSA	Q7F2A7 oryza sativ
48	26	89.7	286	1	AGAY ECOLI	Q42908 escherichia
49	26	89.7	286	2	Q9KIP8 ECOLI	Q9KIP8 escherichia
50	26	89.7	305	2	Q65M26 BALCD	Q65M26 bacillus li
51	26	89.7	313	2	Q5V3J7 HALMD	Q5V3J7 haloarcula
52	26	89.7	327	1	HEMH CHLPN	Q9Z7V1 chlamydia p
53	26	89.7	353	2	Q9TE58 9STRA	Q9TE58 nitazschia f
54	26	89.7	353	2	Q9TE71 9STRA	Q9TE71 cyllindrothe
55	26	89.7	401	2	Q5RH94 BRARE	Q5RH94 brachydanio
56	26	89.7	450	1	PMBA ECOLI	P24231 escherichia
57	26	89.7	450	2	Q7UAN7 SHIFL	Q7UAN7 shigella fl
58	26	89.7	450	2	Q5PJ89 SALPA	Q5PJ89 salmonella
59	26	89.7	450	2	Q7CP84 SALTY	Q7CP84 salmonella
60	26	89.7	450	2	Q8FAP2 ECOLI	Q8FAP2 escherichia
61	26	89.7	450	2	Q8XGJ7 SALTY	Q8XGJ7 salmonella
62	26	89.7	450	2	Q83P54 SHIFL	Q83P54 shigella fl
63	26	89.7	463	2	Q7UKY8 RHOPA	Q7UKY8 rhodopirell
64	26	89.7	473	2	Q57GG4 SALCH	Q57GG4 salmonella
65	26	89.7	478	2	Q5AY52 EMENI	Q5AY52 aspergillus
66	26	89.7	535	2	Q8ERE8 OCEIH	Q8ERE8 oceanobacil
67	26	89.7	552	2	Q4NGJ5 9MICC	Q4NGJ5 arthrobacte
68	26	89.7	583	2	Q9VKE5 DROME	Q9VKE5 drosophila
69	26	89.7	722	2	Q4HYG2 GIBZE	Q4HYG2 gibberella
70	26	89.7	737	2	Q4I160 GIBZE	Q4I160 gibberella
71	26	89.7	947	2	Q5XG9 CRYNE	Q5XG9 cryptococcu
72	26	89.7	1042	2	Q7QXR0 GIALA	Q7QXR0 giardia lam
73	26	89.7	1073	2	Q6GN19 XENLA	Q6GN19 xenopus lae
74	26	89.7	1112	2	Q6QUY1 BRARE	Q6QUY1 brachydanio
75	26	89.7	1127	2	Q7TLR3 BRARE	Q7TLR3 brachydanio
76	26	89.7	1332	2	Q6QUY2 BRARE	Q6QUY2 brachydanio
77	26	89.7	1448	2	Q5R280 DROSE	Q5R280 drosophila
78	26	89.7	1448	2	Q5R284 DROSE	Q5R284 drosophila
79	26	89.7	1449	2	Q9V917 DROME	Q9V917 drosophila
80	26	89.7	1470	2	Q4SNM2 TETNG	Q4SNM2 tetraodon n
81	25	86.2	51	2	Q6ULR1 AOTTR	Q6ULR1 actus trivi
82	25	86.2	66	2	Q4PMR9 IXOST	Q4PMR9 ixodes scap
83	25	86.2	82	2	Q7OTG1 AOTTR	Q7OTG1 actus trivi
84	25	86.2	86	2	Q6UDG1 9HERP	Q6UDG1 psittacid h
85	25	86.2	88	2	Q6Z6M2 ORYSA	Q6Z6M2 oryza sativ
86	25	86.2	93	2	Q8QNH1 9PHYC	Q8QNH1 ectocarpus
87	25	86.2	94	2	P97101 ALCEU	P97101 alcaligenes
88	25	86.2	95	1	CH10 XANAC	P0A0S5 xanthomonas
89	25	86.2	95	1	CH10 XANCP	P0A0R7 xanthomonas
90	25	86.2	95	1	CH10 XANCP	P0A0R6 xanthomonas
91	25	86.2	103	2	Q83913 ENTFA	Q83913 enterococcu
92	25	86.2	107	2	Q4FVP4 9GAMM	Q4FVP4 psychrobact
93	25	86.2	110	2	Q9LJ06 ORYSA	Q9LJ06 oryza sativ
94	25	86.2	111	2	Q4NY28 9DELT	Q4NY28 anaeromyxob
95	25	86.2	119	2	Q7XMD1 ORYSA	Q7XMD1 oryza sativ
96	25	86.2	134	2	Q5GUT0 XANOR	Q5GUT0 xanthomonas
97	25	86.2	138	2	Q22499 CAEEL	Q22499 caenorhabdi
98	25	86.2	143	2	Q4Q885 LEIMA	Q4Q885 leishmania
99	25	86.2	145	2	Q5ZB84 ORYSA	Q5ZB84 oryza sativ
100	25	86.2	145	2	Q5ZB84 ORYSA	Q5ZB84 oryza sativ

ALIGNMENTS

```

RESULT 1
Q9A2W4 CAUCR PRELIMINARY; PRT; 249 AA.
AC Q9A2W4
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hydrolyase, alpha/beta hydrolase fold family.
GN OrderedLocustNames=CC3442;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.P., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Uytterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE006003; AAK25404.1; -; Genomic_DNA.
DR PIR; H87675; H87675.
DR TIGR; CC3442; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b hydrolase.
DR InterPro; IPR003089; AB_hydrolase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00561; ABHYDROLASE_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 249 AA; 26772 MW; 491350127DD300AE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 1 MRAPVI 6

RESULT 2
Q63ZV1 MOUSE PRELIMINARY; PRT; 309 AA.
AC Q63ZV1
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=2310001H13Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082807; AAH82807.1; -; mRNA.
DR MGI; MGI:1914345; 2310001H13Rik.
DR InterPro; IPR000585; Hemopexin.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 309 AA; 32960 MW; 5F551A9B90CC8714 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 286 MRAPVI 291

RESULT 3
Q53093 RHOSH PRELIMINARY; PRT; 442 AA.
AC Q53093
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Flii.
GN Name=flii;
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2 4.1;
RX MEDLINE=96200857; PubMed=8621091; DOI=10.1016/0378-1119(95)00855-1;
RA Ballado T., Campos A., Camarena L., Dreyfus G.;
RT "Flagellar genes from Rhodobacter sphaeroides are homologous to genes
RT of the flii operon of Salmonella typhimurium and to the type-III
RT secretion system.";
RL Gene 170:69-72(1996).
DR EMBL; U31090; BAB07344.1; -; Genomic_DNA.
DR PIR; JC4733; JC4733.
DR HSSP; P03002; LPVO.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0019861; C:flagellum; IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0000158; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0009038; P:biosynthesis; IEA.

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DR GO:0006811; P:ion transport; IEA.
DR GO:0015031; P:protein transport; IEA.
DR InterPro: IPR003593; AAA_ATPase..
DR InterPro: IPR004100; ATPase_a/b_N.
DR InterPro: IPR000194; ATPase_a/b_Centre.
DR InterPro: IPR005714; Flii_YscN.
DR Pfam: PF00006; ATP-synt_ab; 1.
DR SMART: SM00382; AAA; 1.
DR TIGRPFAM: TIGR01026; flii_yscN; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN 1.
SQ SEQUENCE 442 AA; 46852 MW; E6D35531F5A59BAE CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
   |||||
DB 77 MRAPVI 82

RESULT 4
Q53153 RHOSH
ID Q53153_RHOSH PRELIMINARY; PRT; 442 AA.
AC Q53153.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Flii protein.
GN Names=flii;
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS8;
RX MEDLINE=96327148; PubMed=8759796; DOI=10.1016/0378-1097(96)00252-2;
RA Goodfellow I.G., Pollitt C.E., Sockett R.E.;
RT "Cloning of the flii gene from Rhodobacter sphaeroides WS8 by analysis
RT of a transposon mutant with impaired motility.";
RL PMS Microbiol. Lett. 142:111-116(1996).
DR ENBL; X97201; CAA5834.1; -; Genomic_DNA.
DR HSSP; P03002; IPVO.
DR GO:0005737; C:Cytoplasm; IEA.
DR GO:0019861; C:Flagellum; IEA.
DR GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO:0005524; P:ATP binding; IEA.
DR GO:0016887; P:ATPase activity; IEA.
DR GO:0046933; F:hydrogen-transporting ATP synthase activity. . . ; IEA.
DR GO:0046961; F:hydrogen-transporting ATPase activity, rota. . . ; IEA.
DR GO:0016787; F:hydrolyase activity; IEA.
DR GO:0000166; P:nucleotide binding; IEA.
DR GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO:0009058; P:biosynthesis; IEA.
DR GO:0006811; P:ion transport; IEA.
DR GO:0015031; P:protein transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR004100; ATPase_a/b_N.
DR InterPro: IPR000194; ATPase_a/b_Centre.
DR InterPro: IPR005714; Flii_YscN.
DR Pfam: PF00006; ATP-synt_ab; 1.
DR SMART: SM00382; AAA; 1.
DR TIGRPFAM: TIGR01026; flii_yscN; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; UNKNOWN 1.
SQ SEQUENCE 442 AA; 46814 MW; AD070D4E17PD3CC3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
   |||||
DB 77 MRAPVI 82
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DB 77 MRAPVI 82

RESULT 5
O61371 CAEBL
ID O61371_CAEBL PRELIMINARY; PRT; 629 AA.
AC O61371; Q9TX77;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Acetylcholinesterase (EC 3.1.1.7) (Abnormal acetylcholinesterase
DE protein 2).
GN Name=ace-2; ORFNames=Y44E3A.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=N2;
RX MEDLINE=98198570; PubMed=9539167; DOI=10.1016/S0014-5793(98)00191-4;
RA Grauso M., Culetto E., Combes D., Fedon Y., Toutant J.P., Arpagaus M.;
RT "Existence of four acetylcholinesterase genes in the nematodes
RT Caenorhabditis elegans and Caenorhabditis briggsae.";
RL FEBS Lett. 424:279-284(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=N2;
RA Grauso M., Culetto E., Fedon Y., Combes D., Toutant J.P., Arpagaus M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC 1-1 SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR ENBL; AF023378; AAC14016.2; -; mRNA.
DR ENBL; AF106589; AAC78228.2; -; Genomic_DNA.
DR PIR; T33842; T33842.
DR PIR; T37255; T37255.
DR HSSP; P06276; IPQP.
DR Ensembl; Y44E3A.2; Caenorhabditis elegans.
DR WormBase; WBGene0000036; ace-2.
DR WormPep; Y44E3A.2; CE28363.
DR GO:0045202; C:synapse; IEA.
DR GO:0003990; F:acetylcholinesterase activity; IEA.
DR GO:0004104; F:cholinesterase activity; IEA.
DR GO:0016787; F:hydrolyase activity; IEA.
DR GO:0004759; F:serine esterase activity; IEA.
DR GO:0042135; P:neurotransmitter catabolism; IEA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR Complete proteome; Hydrolase; Serine esterase.
SQ SEQUENCE 629 AA; 70864 MW; 74940F512FEDF869 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
   |||||
DB 77 MRAPVI 6

RESULT 6
Q6PD31_MOUSE
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ID AC Q6PD31_MOUSE PRELIMINARY; PRT; 939 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 2310001H13R1k protein.
GN Name=2310001H13R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N.P., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC058971; AAHS8971.1; -, mRNA.
DR Ensembl; ENSMUSG00000032536; Mus musculus.
DR MGI; MGI:1914345; 2310001H13R1k.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR006933; HAP1_N.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF04849; HAP1_N; 1.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
KW Coiled coil; Nuclear protein.
SQ SEQUENCE 939 AA; 104467 MW; 64B1D5D34DF36FCB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 939;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRAPVI 6
Db 916 MRAPVI 921

RESULT 7
Q80TL6_MOUSE PRELIMINARY; PRT; 947 AA.
ID Q80TL6;
AC Q80TL6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKTAA1042 protein (Fragment).
GN Name=2310001H13R1k; Synonyms=mKIAA1042;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22579291; PubMed=12693553;
RX Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:35-48(2003).
DR EMBL; AKI22426; BAC65708.1; -, -.
DR MGI; MGI:1914345; 2310001H13R1k.
DR GO; GO:0005634; C:nucleus; ISS.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0005102; F:receptor binding; ISS.
DR GO; GO:0006493; P:protein amino acid O-linked glycosylation; ISS.
DR GO; GO:0006605; P:protein targeting; ISS.
DR GO; GO:0006357; P:regulation of transcription from RNA polyme. .; ISS.
DR InterPro; IPR006933; HAP1_N.
DR InterPro; IPR000585; Hemopexin.
DR Pfam; PF04849; HAP1_N; 1.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 947 AA; 105487 MW; 0987284C6ACF23A5 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 947;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRAPVI 6
Db 924 MRAPVI 929

RESULT 8
RHBD1_RAT
ID RHBD1_RAT STANDARD; PRT; 164 AA.
AC O85773;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein
DE 1) (Fragment).
GN Name=Rhbd1; Synonyms=Rhbd1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Intestinal epithelium;
RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;
RA Pascall J.C., Brown K.D.;
RT "Characterization of a mammalian cDNA encoding a protein with high
RT sequence similarity to the Drosophila regulatory protein Rhomboid."
RL FEBS Lett. 429:337-340(1998).
CC -!- FUNCTION: May be involved in regulated intramembrane proteolysis
CC and the subsequent release of functional polypeptides from their
CC membrane anchors (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the peptidase S54 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; Y17258; CAA76716.1; -, mRNA.
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DR MEROPS; S54.005; -
DR Ensembl; ENSRNOG00000019921; Rattus norvegicus.
DR InterPro; IPR002610; Rhomboid_1ike.
DR Pfam; PF01694; Rhomboid; 1.
KW Hydrolase; Protease; Serine protease; Transmembrane.
FT TRANSMEM 10 Potential.
FT TRANSMEM 32 52 Potential.
FT TRANSMEM 56 76 Potential.
FT TRANSMEM 120 140 Potential.
FT ACT_SITE 60 60 Charge relay system (By similarity).
FT ACT_SITE 125 125 Charge relay system (By similarity).
FT NON_TER 1 1
FT NON_TER 164 164
SQ SEQUENCE 164 AA; 17662 MW; CF62ACE3B6C99210 CRC64;

Query Match          96.6%; Score 28; DB 1; Length 164;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 52 MRAPVW 57

RESULT 9
Q5TKT1_BRARE
ID Q5TKT1_BRARE PRELIMINARY; PRT; 212 AA.
AC Q5TKT1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Interleukin 17.4.
GN Names=IL-17.4;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RA Irengham G.D., Ram S., Sakai M.;
RT "Cloning and analysis of IL-17 genes in zebrafish.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB195259; BAD72789.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR010345; IL17.
DR Pfam; PF06083; IL17; 1.
SQ SEQUENCE 212 AA; 23624 MW; BFD941CB795D53D CRC64;

Query Match          96.6%; Score 28; DB 2; Length 212;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 1 MRAPVW 6

RESULT 10
Q6FD44_ACIAD
ID Q6FD44_ACIAD PRELIMINARY; PRT; 231 AA.
AC Q6FD44;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=ACIAD1133;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;

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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ADP1;
RX Pubmed=15514110; DOI=10.1093/nar/gkh910;
RA Barbe V., Vallienet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CR543861; CAG68015.1; -; Genomic_DNA.
DR InterPro; IPR007055; TAD.
DR Pfam; PF04972; BON; 1.
DR PROSITE; PS50914; BON; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 231 AA; 24680 MW; 7FCDAFCAFDA5E19F CRC64;

Query Match          96.6%; Score 28; DB 2; Length 231;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 136 MRAPVW 141

RESULT 11
Q4NFV3_9MICC
ID Q4NFV3_9MICC PRELIMINARY; PRT; 359 AA.
AC Q4NFV3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1).
GN ORFNames=ArthDRAFT1826;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAHG0100006; EAL96194.1; -; Genomic_DNA.
KW Oxidoreductase; Pyruvate.
SQ SEQUENCE 359 AA; 38198 MW; 97E6DD01453523BC CRC64;

Query Match          96.6%; Score 28; DB 2; Length 359;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 182 MRAPVW 187

RESULT 12
RHBD1_MOUSE
ID RHBD1_MOUSE STANDARD; PRT; 373 AA.

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AC Q8VC82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein
DE 1).
DE Name=Rbhd1; Synonyms=Rbhd1;
GN Mus musculus
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6; Tissue=Retina;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in regulated intramembrane proteolysis
CC and the subsequent release of functional polypeptides from their
CC membrane anchors (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the peptidase S54 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BC021549; AAH21549.1; -; mRNA.
DR MEGP; S54.005; -.
DR Ensembl; ENSMUSG0000025735; Mus musculus.
DR MGI; MGI:2384891; Rbhd1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR011992; EF-Hand type.
DR InterPro; IPR002610; Rhomboid_1.
DR Pfam; PF01694; Rhomboid; 1.
KW Hydrolase; Protease; Serine protease; Transmembrane.
FT TRANSMEM 131 Potential.
FT TRANSMEM 151 Potential.
FT TRANSMEM 196 Potential.
FT TRANSMEM 219 Potential.
FT TRANSMEM 239 Potential.
FT TRANSMEM 243 Potential.
FT TRANSMEM 275 Potential.
FT TRANSMEM 294 Potential.
FT TRANSMEM 307 Potential.
FT TRANSMEM 327 Potential.
FT TRANSMEM 340 Potential.
FT ACT SITE 199 Charge relay system (By similarity).
FT ACT SITE 247 Charge relay system (By similarity).
FT ACT SITE 312 Charge relay system (By similarity).
FT ACT SITE 312 Charge relay system (By similarity).
SQ SEQUENCE 373 AA; 41786 MW; 1FAE538B3A363D2A CRC64;
Query Match 96.6%; Score 28; DB 1; Length 373;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MRAPV1 6
Db 239 MRAPV 244
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PRT; 376 AA.
Q4UUE2_XANCP PRELIMINARY;
AC Q4UUE2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Flagellar protein.
DE ORFNames=XC_2277;
GN Xanthomonas campestris pv. campestris str. 8004.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=314585;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8004;
RA Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Peng J.-X., Lu L.-F.,
RA Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,
RA Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G.,
RA Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
RA He C.-Z.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000050; AAY49331.1; -; Genomic_DNA.
KW Flagellum.
SQ SEQUENCE 376 AA; 41491 MW; 406778385A158910 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 376;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRAPV1 6
Db 285 MRAPV 290
|||||:
PRT; 376 AA.
Q8P9F5_XANCP PRELIMINARY;
AC Q8P9F5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Flagellar protein.
DE Name=flhB;
GN Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Bertolini M.C.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Cardozo J., Chamberg F.,
RA Camargo L.E.A., Camarotte G., Cannavan F., Coutinho L.L., Cursino-Santos J.R.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Ferreira R.C.C.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
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RT host specificities.;
RL Nature 417:459-463(2002).
DR EMBL: AS012294; AAM41199.1; -; Genomic_DNA.
DR GO: GO:0016020; C.membrane; IEA.
DR GO: GO:0009306; P.protein secretion; IEA.
DR InterPro: IPR006135; Bac.Export_2.
DR InterPro: IPR006136; FlhB.
DR DR PFam: PF01312; Bac export 2; 1.
DR PRINTS: TIGR00328; flhB. 1.
DR TIGRFAMs: TR00950; TYPE3IMPSPROT.
DR Complete proteome; Flagellum.
KW SEQUENCE 376 AA; 41490 MW; 406778385A158910 CRC64;
SQ
Query Match 96.6%; Score 28; DB 2; Length 376;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRAPVI 6
Db 285 MRAPV 290
|||||:

RESULT 15
YTRI_EBV STANDARD; PRT; 425 AA.
AC P30119;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical BTRF1 protein.
GN Name=BTRF1;
OS Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RT Nature 310:207-211(1984).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=82059504; PubMed=7301588;
RA Kozak M.;
RT "Possible role of flanking nucleotides in recognition of the AUG
RT initiator codon by eukaryotic ribosomes.";
RL Nucleic Acids Res. 9:5233-5252(1981).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=83109311; PubMed=6296170;
RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
RT "Sequence analysis and in vitro transcription of portions of the
RT Epstein-Barr virus genome.";
RL J. Cell. Biochem. 19:267-274(1982).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8; PubMed=6300857;
RX MEDLINE=83169725; PubMed=6300857;
RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
RT "Homologous upstream sequences near Epstein-Barr virus promoters.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8; PubMed=6092825;
RX MEDLINE=85035713; PubMed=6092825;
RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
RT Epstein-Barr virus.";
RL Mol. Biol. Med. 1:21-45(1983).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=85060424;
RA Seguin C., Farrell P.J., Barrell B.G.;
RT "DNA sequence and transcription of the BamHI fragment B region of B95-
RT 8 Epstein-Barr virus.";
RL Mol. Biol. Med. 1:369-392(1983).
RN [9]

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BTRF1 protein (Fragment).
GN Name=BTRF1;
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10376;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RT Nature 310:207-211(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=88283646; PubMed=2840285;
RA Laux G., Perricaudet M., Farrell P.J.;
RT "A spliced Epstein-Barr virus gene expressed in immortalized
RT lymphocytes is created by circularization of the linear viral
RT genome.";
RL EMBO J. 7:769-774(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=82014887; PubMed=6269068;
RA Arrand J.R., Rymo L., Walsh J.E., Bjorck E., Lindahl T., Griffin B.E.;
RT "Molecular cloning of the complete Epstein-Barr virus genome as a set
RT of overlapping restriction endonuclease fragments.";
RL Nucleic Acids Res. 9:2999-3014(1981).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=82059504; PubMed=7301588;
RA Kozak M.;
RT "Possible role of flanking nucleotides in recognition of the AUG
RT initiator codon by eukaryotic ribosomes.";
RL Nucleic Acids Res. 9:5233-5252(1981).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=83109311; PubMed=6296170;
RA Deininger P.L., Bankier A., Farrell P., Baer R., Barrell B.;
RT "Sequence analysis and in vitro transcription of portions of the
RT Epstein-Barr virus genome.";
RL J. Cell. Biochem. 19:267-274(1982).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8; PubMed=6300857;
RX MEDLINE=83169725; PubMed=6300857;
RA Farrell P.J., Deininger P.L., Bankier A., Barrell B.;
RT "Homologous upstream sequences near Epstein-Barr virus promoters.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:1565-1569(1983).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8; PubMed=6092825;
RX MEDLINE=85035713; PubMed=6092825;
RA Bankier A.T., Deininger P.L., Farrell P.J., Barrell B.G.;
RT "Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8
RT Epstein-Barr virus.";
RL Mol. Biol. Med. 1:21-45(1983).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=B95-8;
RX MEDLINE=85060424;
RA Seguin C., Farrell P.J., Barrell B.G.;
RT "DNA sequence and transcription of the BamHI fragment B region of B95-
RT 8 Epstein-Barr virus.";
RL Mol. Biol. Med. 1:369-392(1983).
RN [9]

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RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8; PubMed=6310141;
 RX MEDLINE=83294686; PubMed=6310141;
 RA "Organization of the Epstein-Barr virus DNA molecule. III. Location of
 RT the P3HR-1 deletion junction and characterization of the NotI repeat
 RT units that form part of the template for an abundant 12-O-
 RT tetradecanoylphorbol-13-acetate-induced mRNA transcript.";
 RL J. Virol. 48:135-148(1983).
 RN [10]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=85060428; PubMed=6094955;
 RA Bankier A.T., Deininger P.L., Satchwell S.C., Baer R., Farrell P.J.,
 RT "DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-
 RT Barr virus containing the terminal repeat sequences.";
 RL Mol. Biol. Med. 1:425-445(1983).
 RN [11]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=20331131; PubMed=10872327;
 RA Farrell P.J., Bankier A., Seguin C., Deininger P., Bankier B.G.;
 RT "Latent and lytic cycle promoters of Epstein-Barr virus.";
 RL EMBO J. 2:1331-1338(1983).
 RN [12]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=84207939; PubMed=6327290;
 RA Jones M.D., Foster L., Sheedy T., Griffin B.E.;
 RT "The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion
 RT similar to that observed in a non-transforming strain (P3HR-1) of the
 RT virus.";
 RL EMBO J. 3:813-821(1984).
 RN [13]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=84236104; PubMed=6203743;
 RA Biggin M., Farrell P.J., Bankier B.G.;
 RT "Transcription and DNA sequence of the BamHI L fragment of B95-8
 RT Epstein-Barr virus.";
 RL EMBO J. 3:1083-1090(1984).
 RN [14]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=84222045; PubMed=6328526;
 RA Yates J., Warren N., Reisman D., Sugden B.;
 RT "A cis-acting element from the Epstein-Barr viral genome that permits
 RT stable replication of recombinant plasmids in latently infected
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
 RN [15]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=84247360; PubMed=6330697;
 RA Gibson T.J., Stockwell P., Ginsburg M., Bankier B.G.;
 RT "Homology between two EBV early genes and HSV ribonucleotide reductase
 RT and 38K genes.";
 RL Nucleic Acids Res. 12:5087-5099(1984).
 RN [16]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=87289053; PubMed=3039467;
 RA Bodas M., Perricaudet M.;
 RT "Clustered alternative splice sites in Epstein-Barr virus RNAs.";
 RL Nucleic Acids Res. 15:5887-5897(1987).
 RN [17]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RX MEDLINE=91021036; PubMed=2171209;
 RA Parker B.D., Bankier A., Satchwell S., Bankier P.J.;
 RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning
 RT the B95-8 deletion region.";

RL Virology 179:339-346(1990).
 RN [18]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RA Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBSJ databases.
 RN [19]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B95-8;
 RA Binne U.K., Amon W., Farrell P.J.;
 RT "Induction of Epstein-Barr virus late promoters on small plasmids in
 RT the EBV late lytic cycle requires ori lyt.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL: AJ507799; CAD53449.1; -; Genomic_DNA.
 DR InterPro: IPR006772; Herpes_BTRF1.
 DR Pfam: PF04682; Herpes_BTRF1; 1.
 FT NON TER 1
 FT NON TER 425 425
 SQ SEQUENCE 425 AA; 46711 MW; 0ECCBE5FD30495BD CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 425;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 87 MRAPVI 92
 RESULT 17
 RHB1 HUMAN
 ID RHB1_HUMAN STANDARD; PRT; 438 AA.
 AC 075783; Q9NQ85;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Rhomboid-related protein 1 (EC 3.4.21.-) (RRP) (Rhomboid-like protein
 1).
 GN Name=RHB1; Synonyms=RHB1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Leukemia;
 RX MEDLINE=98324821; PubMed=9662444; DOI=10.1016/S0014-5793(98)00622-X;
 RA Pascall J.C., Brown K.D.;
 RT "Characterization of a mammalian cDNA encoding a protein with high
 RT sequence similarity to the Drosophila regulatory protein Rhomboid.";
 RL FEBS Lett. 429:337-340(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).
 RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
 RA Daniels R.J., Peden J.F., Lloyd C., Hordley S.W., Clark K.,
 RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
 RA Higgs D.R.;
 RT "Sequence, structure and pathology of the fully annotated terminal 2
 RT Mb of the short arm of human chromosome 16.";
 RL Hum. Mol. Genet. 10:339-352(2001).
 CC -!- FUNCTION: May be involved in regulated intramembrane proteolysis
 CC and the subsequent release of functional polypeptides from their
 CC membrane anchors (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O75783-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O75783-2; Sequence=VSP_005372;
 CC -!- TISSUE SPECIFICITY: Detected in heart, brain, skeletal muscle and
 CC kidney.

CC -!- SIMILARITY: Belongs to the peptidase S54 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Y17108; CAA76629.1; -; mRNA.
 DR EMBL; AJ272344; CAC00640.1; -; mRNA.
 DR EMBL; AE006464; AAK61241.1; -; Genomic_DNA.
 DR MEROPS; S54.005; -;
 DR Ensembl; ENSG00000103269; Homo sapiens.
 DR HGNC; HGNC:10007; RHBDL1.
 DR MIM; 603264; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005624; C: membrane fraction; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR InterPro; IPR011992; EF-Hand type.
 DR InterPro; IPR002610; Rhomboid-like.
 DR Pfam; PF01694; Rhomboid; 1.
 KW Alternative splicing; Hydrolase; Protease; Serine protease;
 Transmembrane.
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 262 282 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 308 328 Potential.
 FT TRANSMEM 340 359 Potential.
 FT TRANSMEM 372 392 Potential.
 FT TRANSMEM 405 425 Potential.
 FT ACT_SITE 264 264 Charge relay system (By similarity).
 FT ACT_SITE 312 312 Charge relay system (By similarity).
 FT ACT_SITE 377 377 Charge relay system (By similarity).
 FT ACT_SITE 377 377 Charge relay system (By similarity).
 FT VARSPIC 1 77
 FT SOKWEPEPDAPSQPGPALMSRGRTQALAGGSSL -> M
 FT DRSLLOLQIE (in isoform 2).
 FT /FTID:VSP_005372
 SQ SEQUENCE 438 AA; 48314 MW; A7644AD39644A2F6 CRC64;
 Query Match 96.6%; Score 28; DB 1; Length 438;
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 304 MRAPV 309
 RESULT 18
 Q5CWF0_CRYPV Q5CWF0_CRYPV PRELIMINARY; PRT; 486 AA.
 ID Q5CWF0;
 AC Q5CWF0;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=cgdf 5360;
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Iowa type II;
 EX PubMed=15044751; DOI=10.1126/science.1094786;
 RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.,
 RA Lantto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
 RA Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
 RA Anantharaman V., Aravind L., Kapur V.,
 RT "Complete genome sequence of the apicomplexan, Cryptosporidium
 parvum.";
 RL Science 304:441-445 (2004).
 DR EMBL; AAEE01000002; EAK90104.1; -; Genomic_DNA.

DR InterPro; IPR000074; ApoA1_A4_E.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR000471; Interferon abd.
 DR InterPro; IPR004228; Phycoerythr_ab.
 DR InterPro; IPR008976; PLAT_LH2.
 DR InterPro; IPR012288; SlnK/SlnI dimer.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 56469 MW; C632B930E1CAB222 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 486;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 261 MRAPV 266
 RESULT 19
 Q5CG10_CRYHO Q5CG10_CRYHO PRELIMINARY; PRT; 486 AA.
 ID Q5CG10;
 AC Q5CG10;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=Chro.60618;
 OS Cryptosporidium hominis.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=237895;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TU502;
 RA Xu P., Widmer G., Wang Y., Ozaki L.S., Alves J.M., Serrano M.G., P.H.,
 RA Puiu D., Manque P., Akiyoshi D., Mackey A.J., Pearson W.R., Dear P.H.,
 RA Bankier A.T., Peterson D.L., Abrahamson M.S., Kapur V., Tzipori S.,
 RA Buck G.A.,
 RA "The genome of Cryptosporidium hominis.";
 RL Nature 431:1107-1112 (2004).
 DR EMBL; AAEL01000383; EAL35541.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 56527 MW; C8443BDB8159E513 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 486;
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPVI 6
 DB 261 MRAPV 266
 RESULT 20
 Q4S4R8_TETNG Q4S4R8_TETNG PRELIMINARY; PRT; 520 AA.
 ID Q4S4R8;
 AC Q4S4R8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAF14738, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG0024067001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicad S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionnet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Croolins H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA901014738; CAG04364.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 520 AA; 58327 MW; 6C97662B1A77971C CRC64;
Query Match 96.6%; Score 28; DB 2; Length 520;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 386 MRAPV 391
RESULT 21
Q8NT69 CORGL PRELIMINARY; PRT; 541 AA.
AC Q8NT69; Q6W7S9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ResB protein required for cytochrome c biosynthesis (Membrane protein
DE required for cytochrome c biosynthesis).
GN OrderedLocNames=Cg10441, cg0523;
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriidae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
RA Kallinowski J., Bathe B., Bartels D., Eickhoff N., Bott M.,
RA Burkovski A., Dusch N., Eggeling L., Eickmann B.J., Gaigalat L.,
RA Goemann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
RA McHardy A.C., Meyer F., Moeckel B., Pfeifferle W., Puhler A.,
RA Rey D.A., Rueckert C., Rupp O., Salm H., Wendisch V.F., Wiegand I.,
RA Tauch A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins";
RL J. Biotechnol. 104:5-25(2003).
DR EMBL; BA000036; BAB97834.1; -; Genomic DNA.
DR EMBL; BX927149; CAF19157.1; -; Genomic_DNA.
DR InterPro; IPR007816; ResB.
DR Pfam; PF05140; ResB; 1.
KW Complete proteome.

SQ SEQUENCE 541 AA; 61244 MW; 37F42BA0A74F78BB CRC64;
Query Match 96.6%; Score 28; DB 2; Length 541;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 103 MRAPV 108
RESULT 22
Q6CVG6 KUULA PRELIMINARY; PRT; 577 AA.
AC Q6CVG6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.
GN OrderedLocNames=KLU0A00572G;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E., V.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Bolesame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hanraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts";
RL Nature 430:35-44(2004).
DR EMBL; CR32121; CAH02611.1; -; Genomic_DNA.
KW GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 577 AA; 63357 MW; C8E0A541702BD840 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 577;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
DB 364 MRAPV 369
RESULT 23
Q7YYV3 CRYPV PRELIMINARY; PRT; 713 AA.
ID Q7YYV3 CRYPV
AC Q7YYV3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=IMB_818;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Bankier A.T., Spriggs H.F., Partmann B., Konfortov B.A., Madera M.,
 RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 RT *Cryptosporidium parvum*."
 RL Genome Res. 0:0-0(2003).
 DR EMBL; BX538353; CAD98347.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 713 AA; 82980 MW; 101BE54E3C2163CA CRC64;

Query Match 96.6%; Score 28; DB 2; Length 713;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 106 MRAPVI 111

RESULT 24
 ID Q418P3 GIBZE PRELIMINARY; PRT; 152 AA.
 AC Q418P3; 2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE IM17 NEUCR Mitochondrial import inner membrane translocase subunit
 DE TM17.
 GN ORFNames=FG06415.1;
 OS *Gibberella zeae* PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OC NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;

RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Zander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB/2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

Query Match 93.1%; Score 27; DB 2; Length 152;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 54 MRAPVI 59

EMBL; AAC001000257; EAA74619.1; -; Genomic DNA.
 SQ SEQUENCE 152 AA; 15849 MW; A54ABF4244B590CD CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 152;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 ID Q5E5V3 VIBF1 PRELIMINARY; PRT; 179 AA.
 AC Q5E5V3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8).
 GN OrderedLocusNames=VF1098;
 OS *Vibrio fischeri* (strain ATCC 700601 / ES114).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OC NCBI_TaxID=312309;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC PubMed=15703294; DOI=10.1073/pnas.0409900102;
 RA Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M., Gunsalus R.,
 RA Lottroth P., Lupp C., McCann J., Millikan D., Schaefer A., Stabb E.,
 RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
 RT "Complete genome sequence of *Vibrio fischeri*: a symbiotic bacterium
 RT with pathogenic congeners."
 RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
 CC -!- SIMILARITY: Contains 1 pPase cyclophilin-type domain.
 CC EMBL; CF000020; AAW5593.1; -; Genomic DNA.
 DR GO; GO:0016953; F:isomerase activity; IEA.
 DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR002130; CSA_PPIase.
 DR Pfam; PF00160; Pro isomerase; 1.
 DR PRINTS; PR00153; CSA_PPIase; 1.
 DR PROSITE; PS00170; CSA_PPIase_1; 1.
 DR PROSITE; PS00072; CSA_PPIase_2; 1.
 DR Complete proteome; Isomerase; Rotamase.
 KW Complete proteome; Isomerase; Rotamase.
 SQ SEQUENCE 179 AA; 19917 MW; 24A92F9644B53834 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 179;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
 DB 78 MRAPVI 83

RESULT 26
 ID Q51VAV MAGGR PRELIMINARY; PRT; 198 AA.
 AC Q51VAV;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG04228.4;
 OS *Magnaporthe grisea* 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
 OC NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abobe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
 RA Arachi H., Arbruster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,

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RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kellis C., Kleue A., Klenner P., Kodira C., Kulbokas E., Labutski K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marbella R., Maru K., Matthews C., Maucelli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihaliev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoswo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
RA Purcell S., Rachupka T., Ranassamy U., Raneau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tensing P., Tesfaye S., Theodore J., Thoulutseang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACU01001077; EAA50469.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 198 AA; 21159 MW; A8574EAD7237389E CRC64;

Query Match 93.1%; Score 27; DB 2; Length 198;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 54 MRAPVL 59

RESULT 27
O27295_METH PRELIMINARY; PRT; 247 AA.
AC O27295;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Coenzyme PQQ synthesis protein III.
GN OrderedLocuNames=MT1227;
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

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RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
J. Bacteriol. 179:7135-7155(1997).";
RL EMBL; AE000890; AAB85716.1; -; Genomic_DNA.
DR PIR; H69030; H69030.
DR GO; GO:0003824; P: catalytic activity; IEA.
DR GO; GO:0005506; P: iron ion binding; IEA.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF04055; Radical_SAM; 1.
KW Complete proteome.
SQ SEQUENCE 247 AA; 27374 MW; DD1F0C0251DC5217 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 247;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 4 MRAPIV 9

RESULT 28
QSGZK0_XANOR PRELIMINARY; PRT; 333 AA.
ID QSGZK0_XANOR PRELIMINARY;
AC QSGZK0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Flagellar biosynthetic protein FlhB.
GN Name=flhB; OrderedLocuNames=X002617;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KACC10331 / KX085;
RX PubMed=15673718; DOI=10.1093/nar/gki1206;
RA Lee B.-M., Park Y.-J., Park D.-S., Kang H.-W., Kim J.-G., Song E.-S.,
RA Park I.-C., Yoon U.-H., Hahn J.-H., Koo B.-S., Lee G.-B., Kim H.,
RA Park H.-S., Yoon K.-O., Kim J.-H., Jung C.-H., Koh N.-H., Seo J.-S.,
RA Go S.-J.;
RT "The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331,
the bacterial blight pathogen of rice."
RL Nucleic Acids Res. 33:577-586(2005).
DR EMBL; AE013598; AAW5871.1; -; Genomic_DNA.
DR GO; GO:0019861; C: flagellum; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0009306; P: protein secretion; IEA.
DR InterPro; IPR006135; Bac_Export_2.
DR InterPro; IPR006136; FlhB.
DR Pfam; PF01312; Bac_export_2; 1.
DR PRINTS; PR00950; TYPE3IMSPROT.
DR TIGRPFAMs; TIGR00328; flhB; 1.
KW Complete proteome; Flagellum.
SQ SEQUENCE 333 AA; 36513 MW; B06819F9C6A84EE7 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 333;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
Db 242 MRAPIV 247

RESULT 29
Q9L778_XANOR

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ID Q9L778_XANOR PRELIMINARY; PRT; 376 AA.
AC Q9L778_XANOR PRELIMINARY; PRT; 376 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Flagellar biosynthetic protein FlhB.
GN Name=flhB;
OS Xanthomonas oryzae (pv. oryzae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=64187;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21071238; PubMed=11204784;
RX Shen Y.; Chern M.-S.; Silva F.G.; Ronald P.;
RT "Isolation of a Xanthomonas oryzae pv. oryzae flagellar operon region
RL and molecular characterization of flhB."
RL Mol. Plant Microbe Interact. 14:204-213 (2001).
DR EMBL; AP226282; AAF33828.1; -; Genomic_DNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR006135; Bac_Export_2.
DR InterPro; IPR006136; FlhB.
DR Pfam; PF01312; Bac_export_2; 1.
DR PRINTS; PR00950; TYPE3IMSPTOT.
DR TIGRFAMs; TIGR00328; flhB; 1.
KW Flagellum.
SQ SEQUENCE 376 AA; 41154 MW; 68514424C3D1E452 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 285 MRAPIV 290

RESULT 30
ID Q9PL69_XANAC PRELIMINARY; PRT; 376 AA.
AC Q9PL69_XANAC PRELIMINARY; PRT; 376 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Flagellar protein.
GN Name=flhB;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=1204217; DOI=10.1038/417459a;
RA da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;
RA Quaggio R.B.; Monteiro-Vitorello C.B.; Van Sluys M.A.;
RA Almeida N.F. Jr.; Alves L.M.C.; do Amaral A.M.; Bertolini M.C.;
RA Camargo L.E.A.; Camarotte G.; Cannavan F.; Cardozo J.; Chambergo F.;
RA Ciapina L.P.; Ciccarelli R.M.B.; Coutinho L.L.; Cursino-Santos J.R.;
RA El-Dorry H.; Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Gruber A.;
RA Ferro M.I.T.; Formighieri E.F.; Franco M.C.; Greggio C.C.; Lemos M.V.F.;
RA Katsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos B.G.M.; Lemos M.V.F.;
RA Locali E.C.; Machado M.A.; Madeira A.M.B.N.; Martinez-Rossi N.M.;
RA Martins E.C.; Meidanis J.; Menck C.F.M.; Miyaki C.Y.; Moon D.H.;
RA Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;
RA Pereira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;
RA Spinoia L.A.F.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.;
RA Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;
RA Setubal J.C.; Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities."

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RL Nature 417:459-463 (2002).
DR EMBL; AE011829; BAM36799.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR006135; Bac_Export_2.
DR InterPro; IPR006136; FlhB.
DR Pfam; PF01312; Bac_export_2; 1.
DR PRINTS; PR00950; TYPE3IMSPTOT.
DR TIGRFAMs; TIGR00328; flhB; 1.
KW Complete proteome; Flagellum.
SQ SEQUENCE 376 AA; 41333 MW; 615AE986871936AC CRC64;

Query Match 93.1%; Score 27; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 285 MRAPIV 290

RESULT 31
ID Q9ACQ9_STRCO PRELIMINARY; PRT; 416 AA.
AC Q9ACQ9_STRCO PRELIMINARY; PRT; 416 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative transposon transposase.
GN OrderedLocusNames=SCPI.259;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D.; Chater K.F.; Cerdeno-Tarraga A.-M.; Challis G.L.;
RA Thomson N.R.; James K.D.; Harris D.E.; Quail M.A.; Kieser H.;
RA Harper D.; Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.;
RA Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howarth S.;
RA Huang C.-H.; Kieser T.; Larke L.; Murph L.D.; Oliver K.; O'Neill S.;
RA Rabinowitsch E.; Rajandream M.A.; Rutherford K.M.; Rutter S.;
RA Seeger K.; Saunders D.; Sharp S.; Squares R.; Squares S.; Taylor K.;
RA Warren T.; Wietzorrek A.; Woodward J.R.; Barrell B.G.; Parkhill J.;
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL590464; CAC36785.1; -; Genomic DNA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR01207; Trnspase_mutatr.
DR Pfam; PF00872; Transposase mut; 1.
DR PROSITE; PS01007; TRANSPOSASE_MUTATOR; UNKNOWN 1.
KW Complete proteome.
SQ SEQUENCE 416 AA; 45815 MW; 9CBFDD2D33F4B1F2 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 416;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 232 MRAPVL 237

RESULT 32
ID Q4FPU9_9GAMM PRELIMINARY; PRT; 436 AA.
AC Q4FPU9_9GAMM PRELIMINARY; PRT; 436 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE MFS cyanate efflux pump, CynX.
GN Name=CynX; ORFNames=PsyC_2112;
OS Psychrobacter arcticum 273-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=259536;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=273-4;
RG NASA Astrobiology Institute;
RA Ayala-del-Rio H.L., Chain P., Ponder M.A., Di Bartolo G., Ivanova N.,
RA Bergholz P.W., Hauser L., Land M., Bakermans C., Rodrigues D.,
RA Klappenbach J.A., Zarka D., Larimer F., Richardson P., Thomasow M.F.,
RA Tiedje J.M.;
RT "Complete sequence of Psychrobacter arcticum 273-4.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Chain P., Di Bartolo G., Ivanova N., Hauser L.,
RA Land M., Larimer F., Pichuck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, CP000082; AAZ19959.1; -; Genomic DNA.
SQ SEQUENCE 436 AA; 46884 MW; FC50A750C9281789 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 436;
Best Local Similarity 66.7%; Pred. NO. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 60 MRAPV 65

RESULT 33
Q89X81_BRAJA PRELIMINARY; PRT; 449 AA.
AC Q89X81;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blr0433 protein.
GN OrderedLocuNames=blr0433;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Matanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Teurouka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL, BA000040; BAC45698.1; -; Genomic DNA.
DR GO; GO:0004222; F-metalloendopeptidase activity; IEA.
DR GO; GO:0004508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR Pfam; PF01551; Peptidase_M23; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 47625 MW; 0374885B47AB3511 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 449;
Best Local Similarity 83.3%; Pred. NO. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 60 MRAPV 65

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE MFS cyanate efflux pump, CynX.
GN Name=CynX; ORFNames=PsyC_2112;
OS Psychrobacter arcticum 273-4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Psychrobacter.
OX NCBI_TaxID=259536;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=273-4;
RG NASA Astrobiology Institute;
RA Ayala-del-Rio H.L., Chain P., Ponder M.A., Di Bartolo G., Ivanova N.,
RA Bergholz P.W., Hauser L., Land M., Bakermans C., Rodrigues D.,
RA Klappenbach J.A., Zarka D., Larimer F., Richardson P., Thomasow M.F.,
RA Tiedje J.M.;
RT "Complete sequence of Psychrobacter arcticum 273-4.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Chain P., Di Bartolo G., Ivanova N., Hauser L.,
RA Land M., Larimer F., Pichuck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, CP000082; AAZ19959.1; -; Genomic DNA.
SQ SEQUENCE 436 AA; 46884 MW; FC50A750C9281789 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 436;
Best Local Similarity 66.7%; Pred. NO. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 60 MRAPV 65

RESULT 33
Q89X81_BRAJA PRELIMINARY; PRT; 449 AA.
AC Q89X81;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Blr0433 protein.
GN OrderedLocuNames=blr0433;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Matanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Teurouka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL, BA000040; BAC45698.1; -; Genomic DNA.
DR GO; GO:0004222; F-metalloendopeptidase activity; IEA.
DR GO; GO:0004508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR Pfam; PF01551; Peptidase_M23; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 47625 MW; 0374885B47AB3511 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 449;
Best Local Similarity 83.3%; Pred. NO. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 60 MRAPV 65

RESULT 33
Q89TH2_BRARE PRELIMINARY; PRT; 771 AA.
AC Q89TH2;

QY 1 MRAPVI 6
DB 192 MRAPV 197

Query Match 93.1%; Score 27; DB 1; Length 535;
Best Local Similarity 83.3%; Pred. NO. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 192 MRAPV 197

RESULT 34
TLE1_BRARE
ID TLE1_BRARE STANDARD; PRT; 535 AA.
AC O13168;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Groucho 1 protein (Fragment).
GN Name=grol; Synonyms=groucho1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wuelbeck C., Campos-Ortega J.A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Nuclear effector molecule (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Belongs to the WD-repeat Groucho/TLE family.
CC -!- SIMILARITY: Contains 6 WD repeats.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
CC removed.
DR EMBL; Y12467; CAA73070.1; -; mRNA.
DR EMBL; U96451; AAB57808.1; -; mRNA.
DR SMR; O13168; 206-535.
DR Ensembl; ENSDARG00000011822; Danio rerio.
DR ZFIN; ZDB-GENE-990415-85; grol.
DR InterPro; IPR009146; Groucho_enhance.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRINTS; PR01850; GROUCHOFAMLY.
DR ProDom; PD000018; WD40; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS00082; WD_REPEATS_2; 2.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Nuclear protein; Repeat; WD repeat.
FT REPEAT 235 266 WD 1.
FT REPEAT 293 323 WD 2.
FT REPEAT 337 367 WD 3.
FT REPEAT 379 409 WD 4.
FT REPEAT 461 491 WD 5.
FT REPEAT 502 532 WD 6.
FT REGION <1 42 CCN domain.
FT COMPIAS 43 214 Pro/Ser-rich.
FT NON_TER 1
SQ SEQUENCE 535 AA; 57360 MW; A201A32071101363 CRC64;

Query Match 93.1%; Score 27; DB 1; Length 535;
Best Local Similarity 83.3%; Pred. NO. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAPVI 6
DB 192 MRAPV 197

RESULT 35
Q89TH2_BRARE PRELIMINARY; PRT; 771 AA.
AC Q89TH2;
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Groucho-related gene 3 protein.
 GN Name=gr3; Synonyms=grg3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=21294966; PubMed=11401394; DOI=10.1006/dbio.2001.0185;
 RX Kobayashi M., Nishikawa K., Suzuki T., Yamamoto M.;
 RA "The homeobox protein Six3 interacts with the Groucho corepressor and
 RT acts as a transcriptional repressor in eye and forebrain formation.";
 RL Dev. Biol. 232:315-326(2001).
 DR EMBL; AB040707; BAB40698.1; -; mRNA.
 DR HSP; Q04724; IGXR.
 DR SMR; Q98TH2; 442-771.
 DR Ensembl; ENSDARG00000011822; Danio rerio.
 DR ZFIN; ZDB-GENE-010410-1; gr3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0007222; P:frizzled signaling pathway; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR009146; Groucho_enhance.
 DR InterPro; IPR005617; TLE_N.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF03920; TLE_N; 1.
 DR Pfam; PF00400; WD40; 6.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR PRINTS; PR01850; GROUCHOFAMLY.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
 DR PROSITE; PS50082; WD_REPEATS_2; 2.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
 SQ SEQUENCE 771 AA; 83789 MW; 3B9CEB203826E458 CRC64;

 Query Match 93.1%; Score 27; DB 2; Length 771;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MRAPVI 6
 Db 428 MRAPVL 433

 RESULT 36
 Q4UBJ8_SULAC
 ID Q4UBJ8_SULAC PRELIMINARY; PRT; 135 AA.
 AC Q4UBJ8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE CBS domain protein.
 GN OrderedLocNames=Saci 0416;
 OS Sulfolobus acidocaldarius.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2285;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
 RC PubMed=15995215; DOI=10.1128/JB.187.14.4992-4999.2005;
 RX Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
 RA Greve B., Aweyer M., Zibat A., Klenk H.-P., Garrett R.A.;
 RT "The genome of Sulfolobus acidocaldarius, a model organism of the
 Crenarchaeota";
 RL J. Bacteriol. 187:4992-4999(2005).
 RL EMBL; CP000077; AAY79831.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 135 AA; 15028 MW; 0C0A131E252F9D55 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 135;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MRAPVI 6
 Db 15 MRSPVI 20

 RESULT 37
 Q8ILB7_PLAF7
 ID Q8ILB7_PLAF7 PRELIMINARY; PRT; 162 AA.
 AC Q8ILB7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mitochondrial import inner membrane translocase subunit timl7,
 DE putative.
 GN ORFNames=PF14_0328;
 OS Plasmodium falciparum (Isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.G.;
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum";
 RL Nature 419:498-511(2002).
 DR EMBL; AS014821; AN36941.1; -; Genomic_BNA.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.
 DR GO; GO:0015031; P:protein transport; IEA.
 DR InterPro; IPR003397; Timl7_Tim22.
 DR Pfam; PF02466; Timl7; 1.
 SQ SEQUENCE 162 AA; 17909 MW; F536704A462221FF CRC64;

 Query Match 89.7%; Score 26; DB 2; Length 162;
 Best Local Similarity 66.7%; Pred. No. 4.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MRAPVI 6
 Db 58 MRAPIL 63

 RESULT 38
 Q7RLI3_PLAYO
 ID Q7RLI3_PLAYO PRELIMINARY; PRT; 162 AA.
 AC Q7RLI3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mitochondrial import inner membrane translocase subunit timl7.
 GN Name=PY02558;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=17XNL;
 RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RX Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii";
RL Nature 419:512-519(2002).
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABU01000700; EAA22022.1; -; Genomic DNA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0008565; P:protein transporter activity; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR003397; Tim17_Tim22.
DR Pfam; PF02466; Tim17; 1.
SQ SEQUENCE 162 AA; 17956 MW; CAEC647A31E93407 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 58 MRAPIL 63

RESULT 39
Q4XEE4 PLACH PRELIMINARY; PRT; 162 AA.
AC Q4XEE4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit tim17,
DE putative.
GN ORFNames=PC301205.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01007017; CAH84724.1; -; Genomic DNA.
SQ SEQUENCE 162 AA; 17984 MW; 3B23AEH76FF92EB2 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 58 MRAPIL 63

RESULT 40
Q4YVT2 PLABE PRELIMINARY; PRT; 162 AA.
ID Q4YVT2 PLABE PRELIMINARY;

AC Q4YVT2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit tim17,
DE putative.
GN ORFNames=PB000593.02.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01002216; CAH97874.1; -; Genomic DNA.
SQ SEQUENCE 162 AA; 17972 MW; 664BA2ADF3B18B22 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAPVI 6
Db 58 MRAPIL 63

Search completed: November 18, 2005, 21:14:18
Job time : 85.7857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:57:23 ; Search time 63.9286 Seconds
(without alignments)
34.365 Million cell updates/sec

Title: US-10-029-926d-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	5	3	Aay95191 Anti-plat
2	28	100.0	5	5	Abg78239 Human Fv
3	28	100.0	5	5	Abg91930 Human ant
4	28	100.0	5	6	Abu11271 Human TAN
5	28	100.0	5	8	ADI28371 Human CDR
6	28	100.0	5	8	ADs82031 Human scf
7	28	100.0	5	9	Adw77415 Human pla
8	28	100.0	5	9	Adw77403 Human pla
9	28	100.0	10	7	Adm07746 Canine im
10	28	100.0	13	7	Adm75761 Potential
11	28	100.0	13	7	Adm75496 Potential
12	28	100.0	13	7	Adm75231 Potential
13	28	100.0	13	7	Adm75760 Potential
14	28	100.0	13	7	Adm74966 Potential
15	28	100.0	13	7	Adm74967 Potential
16	28	100.0	14	8	Abm79481 Human Fac
17	28	100.0	16	2	Aar49460 Factor VI
18	28	100.0	20	5	ABJ05002 A3 peptid
19	28	100.0	26	1	Abp61435 Factor VI
20	28	100.0	29	1	Aap50314 Peptide e
21	28	100.0	33	1	Aap50318 Peptide e
22	28	100.0	41	1	Aap50313 Thrombin
23	28	100.0	60	5	Abj04948 A3 domain
24	28	100.0	73	3	Aab07206 Human Fac

25	28	100.0	98	3	AAB40073	Aab40073 Anti-hili
26	28	100.0	98	5	ABG78186	Abg78186 Human Fv
27	28	100.0	98	5	ABG91877	Abg91877 Human ant
28	28	100.0	98	6	ABO27087	AbO27087 Human ger
29	28	100.0	98	7	ADF09916	Adf09916 Antibody
30	28	100.0	98	7	ADF10126	Adf10126 Antibody
31	28	100.0	98	7	ADF10024	Adf10024 VEGF anti
32	28	100.0	98	7	ADJ80300	Adj80300 VH gene 1
33	28	100.0	98	9	ADY75305	Ady75305 Protein e
34	28	100.0	98	9	AY95177	Aay95177 Anti-plat
35	28	100.0	113	3	AY95178	Aay95178 Anti-plat
36	28	100.0	115	3	AY95189	Aay95189 Anti-plat
37	28	100.0	115	3	AY95190	Aay95190 Anti-plat
38	28	100.0	116	2	AAW19880	Aaw19880 CEA-speci
39	28	100.0	117	2	AAR66312	Aar66312 Human imm
40	28	100.0	117	9	ADx01783	Adx01783 SARS coro
41	28	100.0	118	4	AU02560	Aau02560 Anti-adip
42	28	100.0	120	2	AR25204	Aar25204 OP-G2 mon
43	28	100.0	123	8	ADJ57861	Adj57861 Light var
44	28	100.0	123	8	AU98019	Aau98019 Human ace
45	28	100.0	207	5	AAP50091	Aap50091 Truncated
46	28	100.0	211	1	AAB07203	Aab07203 Human Fac
47	28	100.0	214	3	AG38412	Aag38412 Arabidops
48	28	100.0	232	7	ABO28086	AbO28086 NPB polyp
49	28	100.0	235	8	ADR28086	Adr28086 NPB polyp
50	28	100.0	236	3	AG29486	Aag29486 Arabidops
51	28	100.0	236	3	AY95198	Aay95198 Anti-plat
52	28	100.0	239	5	ABP46004	Abp46004 Human BLY
53	28	100.0	239	5	ABP46027	Abp46027 Human BLY
54	28	100.0	239	5	ABP44926	Abp44926 Human BLY
55	28	100.0	239	7	ADG95753	Adg95753 Single ch
56	28	100.0	239	7	ADG96854	Adg96854 Single ch
57	28	100.0	239	7	ADG96831	Adg96831 Single ch
58	28	100.0	242	7	ADG30497	Adg30497 Human GMC
59	28	100.0	242	8	ADI58068	Adi58068 Reg IV-sp
60	28	100.0	244	6	AAO31136	Aao31136 Human CM0
61	28	100.0	244	9	ADW90315	Adw90315 Phage scf
62	28	100.0	244	9	ADY01815	Ady01815 SARS coro
63	28	100.0	244	9	ADY34209	Ady34209 TRAIL rec
64	28	100.0	246	5	ABG78329	Abg78329 Human Fv
65	28	100.0	246	5	ABG92026	Abg92026 Antibody
66	28	100.0	249	5	ABF30235	Abf30235 Streptoco
67	28	100.0	249	5	ABG30407	Abg30407 Human GMB
68	28	100.0	251	5	ABP45531	Abp45531 Human BLY
69	28	100.0	251	5	ABP45531	Abp45531 Single ch
70	28	100.0	256	5	ABG78334	Abg78334 Human Fv
71	28	100.0	256	5	ABG78334	Abg78334 Antibody
72	28	100.0	258	7	ADC94375	Adc94375 E. faeciu
73	28	100.0	259	3	AG32033	Aag32033 Arabidops
74	28	100.0	264	5	ADC97186	Adc97186 E. faeciu
75	28	100.0	266	5	ABG92020	Abg92020 Human ant
76	28	100.0	267	3	AG29485	Aag29485 Arabidops
77	28	100.0	267	3	ABF26173	Abf26173 Streptoco
78	28	100.0	268	3	ABG29484	Aag29484 Arabidops
79	28	100.0	268	3	AG32032	Aag32032 Arabidops
80	28	100.0	276	8	ADY22219	Ady22219 Plant ful
81	28	100.0	277	5	ABG78150	Abg78150 Human Fv
82	28	100.0	277	5	ABG78328	Abg78328 Human ant
83	28	100.0	277	5	ABG92019	Abg92019 Human ant
84	28	100.0	277	8	ABG91841	Abg91841 Human ant
85	28	100.0	277	8	ADI28366	Adi28366 Human scf
86	28	100.0	277	8	ADs82026	Ads82026 Human pla
87	28	100.0	279	8	ADx66108	Adx66108 Plant ful
88	28	100.0	300	8	ADx67061	Adx67061 Plant ful
89	28	100.0	309	2	AAW83322	Aaw83322 Single ch
90	28	100.0	309	5	ABO9603	Abb09603 Amino aci
91	28	100.0	309	6	ABG74384	Abg74384 Single ch
92	28	100.0	309	7	ADg98737	Adg98737 Human sin
93	28	100.0	309	8	AD04046	Ado4046 Human sin
94	28	100.0	320	3	AAB07207	Aab07207 Human Fac
95	28	100.0	323	4	AAU69130	Aau69130 Canine ig
96	28	100.0	329	4	AAW70840	Aaw70840 SNV-env 1
97	28	100.0	354	2	AAW54037	Aaw54037 Mouse CC-

98 28 100.0 354 8 ADO29228 Ado29228 Mouse GPC
99 28 100.0 420 4 AAU69122 Aau69122 Canine Ig
100 28 100.0 445 9 ADX02218 Adx02218 SARS coro

ALIGNMENTS

RESULT 1
AA95191
ID AA95191 standard; peptide; 5 AA.
XX
AC AA95191;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human H1b-1 VH CDR1.
XX
KW Variable heavy chain; single chain antibody; scFv; human; H1b-1;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic; CDR1;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
XX WO200026667-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025495.
XX
XX 30-OCT-1998; 98US-0106275P.
XX
XX (MILL) MILLER J L.
XX
XX Miller JL;
XX
XX WPI; 2000-365744/31.
XX
XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
XX Ib alpha molecule useful for producing antibodies which inhibit platelet
XX aggregation.
XX
XX Claim 14; Fig 5; 89pp; English.

The present sequence is that of complementarity determining region 1 (CDR1) of the heavy chain variable region (VH) of human single chain antibody (scFv) H1b-1 (see AA95198), which is directed against platelet glycoprotein Ib (GP1b). The H1b series of scFv was isolated from a human synthetic VH and VL scFv library on the basis of their binding to platelet GP1b. Whether displayed as surface proteins on a phagemid or secreted as free scFv by Escherichia coli, the H1b scFv clones are capable of inhibiting von Willebrand factor-dependent aggregation of platelets. The scFv are composed of native human protein sequences and are therefore attractive potential reagents for therapeutic purposes. They provide a new class of antithrombotic agents, useful for the prevention of platelet-dependent thrombi in diseased arteries, bypass grafts, dialysis etc., and can also be used as diagnostic reagents. Methods of inhibiting aggregation of platelets, of binding human platelet GP1b alpha and of selecting a VH or VL region of an antibody that inhibits platelet aggregation are claimed. Fragments of the scFv VH or VL chain, including CDR fragments, are also claimed

Sequence 5 AA;
Query Match 100.0%; Score 28; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 1 DYGMS 5

RESULT 2
ABG78239
ID ABG78239 standard; peptide; 5 AA.

XX
AC ABG78239;
XX
XX 15-NOV-2002 (first entry)
XX
DE Human Fv molecule hypervariable region related peptide #114.

XX
KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX
OS Homo sapiens.

XX
XX WO200259264-A2.
XX
XX 01-AUG-2002.
XX
XX 31-DEC-2001; 2001WO-US049440.
XX
XX 29-DEC-2000; 2000US-00751181.
XX
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX Plaksin D, Peretz T;
XX
XX WPI; 2002-619166/66.
XX
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX or fragment, or construct of fragment with enhanced binding
XX characteristics so as to selectively bind target cell in favor of other
XX cells.

XX
XX Claim 20; Page 208; 232pp; English.
XX
XX The invention relates to a peptide or polypeptide comprising an Fv
XX molecule, a construct or fragments or a construct of a fragment with
XX enhanced binding characteristics which selectively and/or specifically
XX binds to a target cell in favour of other cells, where binding is
XX primarily determined by a first hypervariable region and Fv is a single
XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX association with or attached, coupled, combined, linked or fused to a
XX pharmaceutical agent, is useful in the manufacture of a medicament, where
XX the medicament has activity against a diseased cell, preferably a cancer
XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX composition for use in inhibiting the growth of a diseased or cancer
XX cell. This sequence represents a human Fv molecule hypervariable region
XX related peptide of the invention

Sequence 5 AA;
Query Match 100.0%; Score 28; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 1 DYGMS 5

RESULT 3
ABG91930
ID ABG91930 standard; peptide; 5 AA.

XX
XX AC ABG91930;
XX
XX 04-DEC-2002 (first entry)
XX
XX

XX Human antibody fragment #114.
DE Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX Homo sapiens.
OS WO200253700-A2.
XX 11-JUL-2002.
XX 31-DEC-2001; 2001WO-US049442.
XX 29-DEC-2000; 2000US-00751181.
XX 29-DEC-2000; 2000US-0258948P.
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.
XX Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX Claim 25; Page 284; Opp; English.
XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX Sequence 5 AA;
XX Query Match 100.0%; Score 28; DB 5; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYGMS 5
DB 1 DYGMS 5
RESULT 4
ID ABU11271
XX ABU11271 standard; peptide; 5 AA.
AC ABU11271;
XX

DT 06-FEB-2003 (first entry)
XX Human TANGO 268 VHCDR1 Peptide #5.
XX Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX Homo sapiens.
OS WO200280968-A1.
XX 17-OCT-2002.
XX 09-APR-2002; 2002WO-US011122.
XX 09-APR-2001; 2001US-00829495.
XX (MILL-) MILLENNIUM PHARM INC.
XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchenker W;
PI Gill DS, Qian DW, Kingsbury G;
XX WPI; 2003-058477/05.
XX Novel substantially purified antibody immunospecifically binding to TANGO
PT 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX Claim 1; Page 111; 236pp; English.
XX This invention relates to a novel purified antibody comprising a variable
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC The antibodies of the invention act to decrease or block TANGO 268
CC binding to extracellular matrix components, or as a collagen or platelet
CC release and aggregation blocker. The antibodies of the invention are
CC useful for modulating proliferation, migration, morphology,
CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degranulation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such
CC as thrombocytopenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only caused a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention
XX Sequence 5 AA;
XX Query Match 100.0%; Score 28; DB 6; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 1 DYGMS 5

RESULT 5
ADI28371
ID ADI28371 standard; peptide; 5 AA.
XX AC ADI28371;
XX DT 06-MAY-2004 (first entry)
XX DE Human CDR1 peptide, used in therapeutic composition.
XX KW Human; antibody; scFv; complementarity determining region; drug delivery;
XX KW cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX PA (SAVI-) SAVIENT PHARM INC.
XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX WPI; 2004-099189/10.
XX Composition comprising an agent and/or antibody or its fragment, useful
PT for treating auto-immune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.
XX Claim 15; SEQ ID NO 6; 58pp; English.

CC The present sequence is that of a human antibody complementarity
CC determining region 1 (CDR1). The invention relates to compositions
CC utilising an agent and an antibody or its fragment. The agent is a toxin,
CC radioisotope or pharmaceutical agent such as doxorubicin. It is complexed
CC or combined with or conjugated to the antibody or its fragment. The
CC antibody may have a first hypervariable region comprising a CDR3, a
CC second hypervariable region comprising a CDR2 and a third hypervariable
CC sequence comprising the present CDR1 sequence. The agent and/or antibody
CC can be present in the composition is a sub-clinical amount, i.e. less
CC than the amount generally found to be clinically effective when the agent
CC is administered alone. The composition is used in claimed methods of:
CC inhibiting cell rolling, inflammation, thrombosis, restenosis,
CC metastasis, the growth and/or replication of tumour cells or leukaemia
CC cells, an increase in number of tumour or leukaemia cells, cell-cell,
CC cell-matrix, platelet-matrix, platelet-platelet and/or cell-platelet
CC complex formation, aggregation or adhesion; increasing the mortality rate
CC of tumour or leukaemia cells, the susceptibility of disease cells to
CC damage by anti-disease agents, and the susceptibility of tumour or
CC leukaemia cells to damage by anti-cancer agents; and ameliorating the
CC effects of a disease, preventing a disease, treating a disease or
CC inhibiting the progress of a disease.

XX Sequence 5 AA;
Query Match 100.0%; Score 28; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 1 DYGMS 5

RESULT 6
ADS82031
ID ADS82031 standard; peptide; 5 AA.
XX AC ADS82031;
XX DT 30-DEC-2004 (first entry)
XX DE Human scFv antibody CDR1 hypervariable region SEQ ID NO 6.
XX KW cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
XX KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
XX KW human; scFv; antibody; cytostatic; anti-inflammatory; thrombolytic;
XX KW vasotropic; immunosuppressive; cardiovascular-Gen; ophthalmological.
XX OS Homo sapiens.
XX PN US2004202665-A1.
XX PD 14-OCT-2004.
XX PF 30-JUN-2003; 2003US-00610843.
XX PR 01-JUL-2002; 2002US-0393453P.
XX PA (LAZA/) LAZAROVITS J.
XX PA (NIMR/) NIMROD A.
XX PA (HOCH/) HOCH M H.
XX PA (LEVA/) LEVANON A.
XX PI Lazarovits J, Nimrod A, Hoch MH, Levanon A;
XX WPI; 2004-746943/73.
XX Composition useful for treating diseases e.g., inflammatory diseases,
PT thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
PT retinopathic diseases, comprises agent and antibody or its fragment.
XX Disclosure; SEQ ID NO 6; 22pp; English.

CC The invention relates to a composition which comprises an agent and an
CC antibody or its fragment. The composition is useful for inhibiting cell
CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
CC and/or cell-platelet complex formation, aggregation or adhesion, increase
CC in number of tumour cells or growth and/or replication of tumour or
CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
CC ameliorating the effect of a disease, preventing a disease, treating a
CC disease, or inhibiting the progress of a disease. The composition is
CC useful for therapeutic treatment, where antibody or its fragment and the
CC agent are administered separately. The antibody or its fragment is
CC administered prior to or subsequent to the agent. The composition is
CC useful for treating diseases such as inflammatory diseases, diseases
CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
CC diseases involving abnormal or pathogenic aggregation, autoimmune
CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
CC by sulphated tyrosine-dependent protein-protein interactions or diseased
CC cells. The present sequence represents a human scFv antibody CDR1
CC hypervariable region.

XX Sequence 5 AA;
Query Match 100.0%; Score 28; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 1 DYGMS 5

RESULT 7

ADW77415

ID ADW77415 standard; peptide; 5 AA.

XX AC ADW77415;

XX DT 07-APR-2005 (first entry)

XX DE

XX DE Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 86.

XX KW Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;

XX KW Ophthalmological; Immunosuppressive; Vasotropic; antibody;

XX KW platelet membrane glycoprotein VI; diabetic retinopathy;

XX KW cardiovascular disease; ocular disease; graft versus host disease;

XX KW immune disorder.

XX OS Homo sapiens.

XX OS WO2005007800-A2.

XX PN 27-JAN-2005.

XX PF 20-JUL-2004; 2004WO-JP010596.

XX PR 18-JUL-2003; 2003JP-00199192.

XX XX (MOCH) MOCHIDA PHARM CO LTD.

XX PA Takayama H, Shirakawa K, Yamakawa T, Kawahara T;

XX PI WPI; 2005-152077/16.

XX DR Novel human antibody or its active fragment capable of binding

XX PT specifically with human platelet membrane glycoprotein VI and not

XX PT inducing human platelet aggregation by itself, useful for treatment or

XX PT prevention of thrombosis.

XX PS Example 8; SEQ ID NO 86; 124pp; Japanese.

XX CC The invention relates to a human antibody or its active fragment capable

XX CC of binding specifically with human platelet membrane glycoprotein VI and

XX CC not inducing human platelet aggregation by itself. The antibody is useful

XX CC in treatment or prevention of thrombosis, embolism or arteriosclerosis.

XX CC The antibody is useful in diagnosis of the disease by detecting or

XX CC determining glycoprotein VI. The antibody is useful in the prevention

XX CC and/or treatment of vascular endothelium failure, vascular endothelium

XX CC hyperthrophy, blood vessel restenosis, disseminated intravascular

XX CC coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.

XX CC The antibody exhibits high specificity with respect to glycoprotein VI,

XX CC and can be obtained easily. The present sequence represents the amino

XX CC acid sequence of a human platelet membrane glycoprotein VI associated

XX CC CDR.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 28; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. NO. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

DB 1 DYGMS 5

RESULT 8

ADW77403

ID ADW77403 standard; peptide; 5 AA.

XX AC ADW77403;

XX DT 07-APR-2005 (first entry)

XX DE

XX DE Canine immunoglobulin heavy chain variable domain CDR1 peptide 14.

XX KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

XX KW antiallergic; allergy; IgE; gene therapy;

XX KW complementarity determining region; CDR1.

XX OS Canis familiaris.

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PN WO2003060080-A2.
 XX 24-JUL-2003.
 XX 20-DEC-2002; 2002WO-US041362.
 XX 21-DEC-2001; 2001US-0344874P.
 XX (IDEX-) IDEX LAB INC.
 XX Krah ER, Guo H, Aiyappa A, Lawton R;
 XX WPI; 2003-598521/56.
 XX New canine heavy and light chain variable domain polypeptides, useful for
 XX treating canine allergy.
 XX Claim 15; Page 95; 130pp; English.
 XX The invention relates to a novel canine heavy or light chain variable
 XX domain polypeptide. The protein of the invention demonstrates
 XX antiallergic activity and may be useful for treating canine allergy,
 XX possibly via gene therapy. The current sequence is that of a canine
 XX immunoglobulin heavy chain variable domain complementarity determining
 XX region (CDR) peptide of the invention.
 XX SQ Sequence 10 AA;
 Query Match 100.0%; Score 28; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 6 DYGMS 10
 RESULT 10
 ADM75761
 ID ADM75761 standard; peptide; 13 AA.
 AC ADM75761;
 XX 03-JUN-2004 (first entry)
 DT Potential human MHC class II binding human Factor VIII peptide #981.
 XX human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 XX MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX Homo sapiens.
 OS WO2003087161-A1.
 PN 23-OCT-2003.
 PD 17-APR-2003; 2003WO-EP004063.
 XX 18-APR-2002; 2002EP-00008712.
 XX 24-MAR-2003; 2003EP-00006554.
 XX (MERE) MERCK PATENT GMBH.
 XX Jones T, Baker M, Carr FJ;
 XX WPI; 2003-845307/78.
 XX New modified human Factor VIII molecule being substantially non-
 XX immunogenic or less immunogenic than non-modified human Factor VIII,
 XX useful in preparing a composition for treating e.g., Gaucher's disease.
 XX Disclosure; Fig 1; 68pp; English.

CC The invention relates to a novel modified human Factor VIII molecule. The
 CC modified human Factor VIII molecule being substantially non-immunogenic
 CC or less immunogenic than a non-modified human Factor VIII and having
 CC essentially the same biological specificity and activity when used in
 CC vivo. The modified human Factor VIII molecule comprises specifically
 CC altered amino acid residues compared with the non-modified parental
 CC molecule, where the altered amino acid residues cause a reduction or an
 CC elimination of one or more of the T-cell epitopes, which act in the
 CC parental non-modified molecule as MHC class II binding ligands and
 CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.
 XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 3 DYGMS 7
 RESULT 11
 ADM75496
 ID ADM75496 standard; peptide; 13 AA.
 XX ADM75496;
 XX 03-JUN-2004 (first entry)
 DT Potential human MHC class II binding human Factor VIII peptide #716.
 XX human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
 XX MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
 XX Homo sapiens.
 OS WO2003087161-A1.
 PN 23-OCT-2003.
 PD 17-APR-2003; 2003WO-EP004063.
 XX 18-APR-2002; 2002EP-00008712.
 XX 24-MAR-2003; 2003EP-00006554.
 XX (MERE) MERCK PATENT GMBH.
 XX Jones T, Baker M, Carr FJ;
 XX WPI; 2003-845307/78.
 XX New modified human Factor VIII molecule being substantially non-
 XX immunogenic or less immunogenic than non-modified human Factor VIII,
 XX useful in preparing a composition for treating e.g., Gaucher's disease.
 XX Disclosure; Fig 1; 68pp; English.
 XX The invention relates to a novel modified human Factor VIII molecule. The
 XX modified human Factor VIII molecule being substantially non-immunogenic
 XX or less immunogenic than a non-modified human Factor VIII and having
 XX essentially the same biological specificity and activity when used in
 XX vivo. The modified human Factor VIII molecule comprises specifically
 XX altered amino acid residues compared with the non-modified parental
 XX molecule, where the altered amino acid residues cause a reduction or an
 XX elimination of one or more of the T-cell epitopes, which act in the
 XX parental non-modified molecule as MHC class II binding ligands and

CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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 Db 4 DYGMS 8

RESULT 12

ADM75231
 ID ADM75231 standard; peptide; 13 AA.

XX AC ADM75231;

XX DT 03-JUN-2004 (first entry)

XX DE Potential human MHC class II binding human Factor VIII peptide #451.

XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;

XX KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX OS Homo sapiens.

XX PN WO2003087161-A1.

XX PD 23-OCT-2003.

XX PF 17-APR-2003; 2003WO-EP004063.

XX PR 18-APR-2002; 2002EP-00008712.

XX PR 24-MAR-2003; 2003EP-00006554.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Jones T, Baker M, Carr FJ;

XX DR WPI; 2003-845307/78.

XX PT New modified human Factor VIII molecule being substantially non-
 PT immunogenic or less immunogenic than non-modified human Factor VIII,
 PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX PS Disclosure; Fig 1; 68pp; English.

XX CC The invention relates to a novel modified human Factor VIII molecule. The
 CC modified human Factor VIII molecule being substantially non-immunogenic
 CC or less immunogenic than a non-modified human Factor VIII and having
 CC essentially the same biological specificity and activity when used in
 CC vivo. The modified human Factor VIII molecule comprises specifically
 CC altered amino acid residues compared with the non-modified parental
 CC molecule, where the altered amino acid residues cause a reduction or an
 CC elimination of one or more of the T-cell epitopes, which act in the
 CC parental non-modified molecule as MHC class II binding ligands and
 CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 5 DYGMS 9

RESULT 13

ADM75760
 ID ADM75760 standard; peptide; 13 AA.

XX AC ADM75760;

XX DT 03-JUN-2004 (first entry)

XX DE Potential human MHC class II binding human Factor VIII peptide #980.

XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;

XX KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX OS Homo sapiens.

XX PN WO2003087161-A1.

XX PD 23-OCT-2003.

XX PF 17-APR-2003; 2003WO-EP004063.

XX PR 18-APR-2002; 2002EP-00008712.

XX PR 24-MAR-2003; 2003EP-00006554.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Jones T, Baker M, Carr FJ;

XX DR WPI; 2003-845307/78.

XX PT New modified human Factor VIII molecule being substantially non-
 PT immunogenic or less immunogenic than non-modified human Factor VIII,
 PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX PS Disclosure; Fig 1; 68pp; English.

XX CC The invention relates to a novel modified human Factor VIII molecule. The
 CC modified human Factor VIII molecule being substantially non-immunogenic
 CC or less immunogenic than a non-modified human Factor VIII and having
 CC essentially the same biological specificity and activity when used in
 CC vivo. The modified human Factor VIII molecule comprises specifically
 CC altered amino acid residues compared with the non-modified parental
 CC molecule, where the altered amino acid residues cause a reduction or an
 CC elimination of one or more of the T-cell epitopes, which act in the
 CC parental non-modified molecule as MHC class II binding ligands and
 CC stimulate T-cells. The potential MHC class II binding activity peptide is
 CC useful for the manufacture of the modified Factor VIII molecule or a
 CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.
 CC The modified Factor VIII molecule is useful in preparing a composition
 CC for treating e.g., Gaucher's disease. This sequence represents a human
 CC Factor VIII peptide with potential human MHC class II binding activity of
 CC the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||
 Db 9 DYGMS 13

RESULT 14

ADM74966
ID ADM74966 standard; peptide; 13 AA.

XX AC ADM74966;

XX DT 03-JUN-2004 (first entry)

XX DE Potential human MHC class II binding human Factor VIII peptide #186.

XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;

XX KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX OS Homo sapiens.

XX PN WO2003087161-A1.

XX PD 23-OCT-2003.

XX PF 17-APR-2003; 2003WO-EP004063.

XX PR 18-APR-2002; 2002EP-00008712.

XX PR 24-MAR-2003; 2003EP-00006554.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Jones T, Baker M, Carr FJ;

XX DR WPI; 2003-845307/78.

XX PT New modified human Factor VIII molecule being substantially non-

XX PT immunogenic or less immunogenic than non-modified human Factor VIII,

XX PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX PS Disclosure; Fig 1; 68pp; English.

XX CC The invention relates to a novel modified human Factor VIII molecule. The

XX CC modified human Factor VIII molecule being substantially non-immunogenic

XX CC or less immunogenic than a non-modified human Factor VIII and having

XX CC essentially the same biological specificity and activity when used in

XX CC vivo. The modified human Factor VIII molecule comprises specifically

XX CC altered amino acid residues compared with the non-modified parental

XX CC molecule, where the altered amino acid residues cause a reduction or an

XX CC elimination of one or more of the T-cell epitopes, which act in the

XX CC parental non-modified molecule as MHC class II binding ligands and

XX CC stimulate T-cells. The potential MHC class II binding activity peptide is

XX CC useful for the manufacture of the modified Factor VIII molecule or a

XX CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.

XX CC The modified Factor VIII molecule is useful in preparing a composition

XX CC for treating e.g., Gaucher's disease. This sequence represents a human

XX CC Factor VIII peptide with potential human MHC class II binding activity of

XX CC the invention.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5

|||||

8 DYGMS 12

RESULT 15

ADM74967
ID ADM74967 standard; peptide; 13 AA.

XX AC ADM74967;

XX DT 03-JUN-2004 (first entry)

XX

DE Potential human MHC class II binding human Factor VIII peptide #187.

XX KW human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;

XX KW MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.

XX OS Homo sapiens.

XX PN WO2003087161-A1.

XX PD 23-OCT-2003.

XX PF 17-APR-2003; 2003WO-EP004063.

XX PR 18-APR-2002; 2002EP-00008712.

XX PR 24-MAR-2003; 2003EP-00006554.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Jones T, Baker M, Carr FJ;

XX DR WPI; 2003-845307/78.

XX PT New modified human Factor VIII molecule being substantially non-

XX PT immunogenic or less immunogenic than non-modified human Factor VIII,

XX PT useful in preparing a composition for treating e.g., Gaucher's disease.

XX PS Disclosure; Fig 1; 68pp; English.

XX CC The invention relates to a novel modified human Factor VIII molecule. The

XX CC modified human Factor VIII molecule being substantially non-immunogenic

XX CC or less immunogenic than a non-modified human Factor VIII and having

XX CC essentially the same biological specificity and activity when used in

XX CC vivo. The modified human Factor VIII molecule comprises specifically

XX CC altered amino acid residues compared with the non-modified parental

XX CC molecule, where the altered amino acid residues cause a reduction or an

XX CC elimination of one or more of the T-cell epitopes, which act in the

XX CC parental non-modified molecule as MHC class II binding ligands and

XX CC stimulate T-cells. The potential MHC class II binding activity peptide is

XX CC useful for the manufacture of the modified Factor VIII molecule or a

XX CC vaccine in order to reduce immunogenicity to Factor VIII in a patient.

XX CC The modified Factor VIII molecule is useful in preparing a composition

XX CC for treating e.g., Gaucher's disease. This sequence represents a human

XX CC Factor VIII peptide with potential human MHC class II binding activity of

XX CC the invention.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 28; DB 7; Length 13;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5

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2 DYGMS 6

RESULT 16

ABM79481
ID ABM79481 standard; peptide; 14 AA.

XX AC ABM79481;

XX DT 22-APR-2004 (first entry)

XX

DE Human Factor VIII peptide fragment SEQ ID NO: 5.

XX KW Antibody; human; Factor VIII; LRP; haemostatic; haemophilia A;

XX KW low-density lipoprotein receptor-related protein;

XX KW blood coagulation disorder.

XX OS Homo sapiens.

XX PN WO2003093313-A2.

CC thereof, as well as DNA encoding those peptides, useful to prevent or
 CC treat antibody inhibitors of factor VIII. The peptides are useful for
 CC preventing or inhibiting aberrant, pathogenic or undesirable antibody
 CC production or antibody binding that is specific for factor VIII. The
 CC peptides are also useful for preventing or inhibiting the priming or
 CC activity of T cells specific for factor VIII. These peptides are also
 CC useful for enhancing the activity or increasing the levels of modulatory
 CC T cells that inhibit the immune response to factor VIII. These peptides
 CC are useful in mammals, particularly in humans. The administration of
 CC these peptides does not increase the synthesis of a pathogenic antibody
 CC to factor VIII, or its biologically active fragment or functional
 CC equivalent. In particular, these peptides are useful for treating
 CC haemophilia A or acquired haemophilia. This sequence represents a human
 CC factor VIII peptide region relating to the invention
 XX
 XX SQ Sequence 20 AA;
 Query Match 100.0%; Score 28; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 9 DYGMS 13
 |||||
 RESULT 19
 AAP61435
 ID AAP61435 standard; protein; 26 AA.
 XX
 AC AAP61435;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-AUG-1991 (first entry)
 XX
 XX Factor VIII:C coagulant polypeptide.
 DE
 XX Factor VIII:C; coagulant; haemophilia; clotting; blood.
 KW
 XX Homo sapiens.
 OS
 XX EPI82372-A.
 PN
 XX 28-MAY-1986.
 XX
 XX 19-NOV-1985; 85EP-00114743.
 PF
 XX 31-MAR-1983; 83US-00481105.
 PR 30-NOV-1983; 83US-00556508.
 PR 21-NOV-1984; 84US-00673916.
 PR 24-MAY-1985; 85US-00738134.
 PR 13-APR-1987; 87US-00037615.
 XX
 XX (SCRI) SCRIPPS CLINIC & RES FOUND.
 PA
 XX Zimmermann TS, Fulcher CA;
 PI
 XX WPI; 1986-138803/22.
 XX
 XX New factor VIII:c coagulant polypeptide(s) - useful for enhanced activity
 PT in treating haemophilia and obtd. by treating factor VIII:c with
 PT protease.
 XX
 XX Claim 6; Page 44; 46pp; English.
 PS
 CC The polypeptide has mol. wt. of approx. 79000-80000. It is an active
 CC Factor VIII:C coagulant polypeptide, and has enhanced coagulant activity.
 CC It is useful for treating haemophilia. It is also useful in the study and
 CC characterisation of polypeptides or their complexes providing desired
 CC clotting behaviour in the blood of humans and other mammals. Activity may
 CC be 3-5 times that of known purified human Factor VIII:C, or even 10-100
 CC times. Activity is shown over a continuous period of at least 10 mins.,
 CC and usually for much longer. The polypeptide may be mixed with other

CC Factor VIII:C polypeptides to produce a specific coagulant activity of
 CC over 1000 units/ml. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX SQ Sequence 26 AA;
 Query Match 100.0%; Score 28; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 19 DYGMS 23
 |||||
 RESULT 20
 AAP50314
 ID AAP50314 standard; protein; 29 AA.
 XX
 AC AAP50314;
 XX
 XX 25-MAR-2003 (revised)
 DT 23-NOV-1991 (first entry)
 XX
 XX Peptide encoded by porcine antihaemophilic factor exon (34-H1).
 DE
 XX Porcine antihaemophilic factor; haemophilia; factor VIIIC.
 KW
 XX Sus scrofa.
 OS
 XX W08501961-A.
 PN
 XX 09-MAY-1985.
 PD
 XX 12-OCT-1984; 84WO-US001641.
 PF
 XX 28-OCT-1983; 83US-00546650.
 PR 24-AUG-1984; 84US-00644036.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Toole J;
 PI
 XX WPI; 1985-122479/20.
 XX
 XX Prodn. of human and porcine factor VIIIC - by using recombinant dna
 PT techniques for their cellular prodn.
 PT
 XX Disclosure; Fig 1B; 71pp; English.
 PS
 XX The peptide is encoded by an exon of the porcine antihaemophilic factor
 CC (AHF) gene. The exon, from nucleotides 169 to 267, encodes at least 30
 CC amino acids from Phe 2 to Arg 31 of the 69 kD fragment. The AHF was obtd.
 CC using anti-factor VIIIC monoclonal antibody. The peptide is useful for
 CC the treatment of haemophilia. (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX SQ Sequence 29 AA;
 Query Match 100.0%; Score 28; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 20 DYGMS 24
 |||||
 RESULT 21
 AAP50318
 ID AAP50318 standard; protein; 33 AA.
 XX
 AC AAP50318;
 XX

DT 25-MAR-2003 (revised)
 DT 23-NOV-1991 (first entry)
 XX Peptide encoded by HaeIII insert 34-HI bearing porcine antihaemophilic
 DE factor exon.
 XX Porcine antihaemophilic factor; haemophilia; insert 34-HI; factor VIIIc.
 KW Sus scrofa.
 XX
 OS Key Location/Qualifiers
 FH Region 3..33
 FT /label= human factor VIIIc sequence
 XX
 XX WO8501961-A.
 PN
 XX 09-MAY-1985.
 PD
 XX 12-OCT-1984; 84WO-US001641.
 XX
 XX 28-OCT-1983; 83US-00546650.
 PR
 XX 24-AUG-1984; 84US-00644036.
 XX
 XX (GEM) GENETICS INST INC.
 PA
 XX Toole J;
 PI
 XX WPI; 1985-122479/20.
 DR
 XX N-PSDB; AAN50373.
 DR
 XX Prodn. of human and porcine factor VIIIc - by using recombinant dna
 PT techniques for their cellular prodn.
 PT
 XX Disclosure; Fig 5; 71pp; English.
 PS
 XX The peptide is encoded by the HaeIII insert 34-HI, which bears the exon
 CC for porcine antihaemophilic factor (AHF). It contains a portion of human
 CC factor VIIIc. The nucleotide sequence encoding this human region
 CC (claimed) can be used as a screening agent to identify DNA and RNA
 CC sequences encoding at least part of the human factor VIIIc gene. Human
 CC factor VIIIc and porcine AHF are useful for the treatment of haemophilia.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 XX Sequence 33 AA;
 SQ
 Query Match 100.0%; Score 28; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 20 DYGMS 24
 RESULT 22
 AAP50313
 ID AAP50313 standard; peptide; 41 AA.
 XX
 AC AAP50313;
 XX
 XX 25-MAR-2003 (revised)
 DT 23-NOV-1991 (first entry)
 XX
 XX Thrombin cleavage prod. of porcine antihaemophilic factor.
 DE
 XX Porcine antihaemophilic factor; haemophilia; thrombin cleavage prod;
 KW factor VIIIc.
 XX
 XX Sus scrofa.
 OS
 XX WO8501961-A.
 PN
 XX

PD 09-MAY-1985.
 XX 12-OCT-1984; 84WO-US001641.
 XX 28-OCT-1983; 83US-00546650.
 PR 24-AUG-1984; 84US-00644036.
 XX (GEM) GENETICS INST INC.
 PA
 XX Toole J;
 PI
 XX WPI; 1985-122479/20.
 DR
 XX Prodn. of human and porcine factor VIIIc - by using recombinant dna
 PT techniques for their cellular prodn.
 PT
 XX Disclosure; Fig 1A; 71pp; English.
 PS
 XX The peptide is the N-terminal sequence of the 69 kD thrombin cleavage
 CC prod. of porcine antihaemophilic factor (AHF). The AHF was obtd. using
 CC anti-factor VIIIc monoclonal antibody. The peptide is useful for the
 CC treatment of haemophilia. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 41 AA;
 SQ
 Query Match 100.0%; Score 28; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 DB 18 DYGMS 22
 RESULT 23
 ABJ04948
 ID ABJ04948 standard; protein; 60 AA.
 XX
 AC ABJ04948;
 XX
 XX 30-OCT-2002 (first entry)
 DT
 XX A3 domain of fVII epitope SEQ ID No 4.
 DE
 XX Haemostatic; antibody inhibitor; factor VIII; T cell; immune response;
 KW haemophilia A; acquired haemophilia; human factor VIII.
 XX
 XX Homo sapiens.
 OS
 XX WO200260917-A2.
 PN
 XX 08-AUG-2002.
 PD
 XX 30-NOV-2001; 2001WO-US044945.
 PF
 XX 01-DEC-2000; 2000US-0250430P.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA
 XX Conti-Fine BM;
 PI
 XX WPI; 2002-627462/67.
 DR
 XX New peptides or their variants, useful for preventing, treating or
 PT inhibiting aberrant or pathogenic production of antibodies specific for
 PT factor VIII, particularly useful for treating hemophilia A or acquired
 PT hemophilia.
 XX
 XX Claim 4; Page 84; 120pp; English.
 PS
 XX The invention relates to isolated and purified peptides and variants
 CC thereof, as well as DNA encoding those peptides, useful to prevent or

CC treat antibody inhibitors of factor VIII. The peptides are useful for
 CC preventing or inhibiting aberrant, pathogenic or undesirable antibody
 CC production or antibody binding that is specific for factor VIII. The
 CC peptides are also useful for preventing or inhibiting the priming or
 CC activity of T cells specific for factor VIII. These peptides are also
 CC useful for enhancing the activity or increasing the levels of modulatory
 CC T cells that inhibit the immune response to factor VIII. These peptides
 CC are useful in mammals, particularly in humans. The administration of
 CC these peptides does not increase the synthesis of a pathogenic antibody
 CC to factor VIII, or its biologically active fragment or functional
 CC equivalent. In particular, these peptides are useful for treating
 CC haemophilia A or acquired haemophilia. This sequence represents a human
 CC factor VIII protein region relating to the invention

XX SQ Sequence 60 AA;

Query Match 100.0%; Score 28; DB 5; Length 60;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYQMS 5
 Db 39 DYQMS 43
 |||||

RESULT 24
 AAB07206
 ID AAB07206 standard; protein; 73 AA.

XX AC AAB07206;

XX DT 11-OCT-2000 (first entry)

XX DE Human Factor VIII C domain; human; blood clotting; haemophilia.

XX KW Factor VIII C domain; human; blood clotting; haemophilia.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 53
 XX FT /note= "encoded by CGT"

XX EP1006182-A2.

XX PD 07-JUN-2000.

XX PF 11-JAN-1985; 2000EP-00200860.

XX PR 12-JAN-1984; 84US-00570062.

XX PR 26-OCT-1984; 84US-00664919.

XX PR 11-JAN-1985; 85EP-00100223.

XX PR 11-JAN-1985; 91EP-00113267.

XX (CHIR) CHIRON CORP.

XX FA (NOVO) NOVO-NORDISK AS.

XX PI Kuo G, Rasmussen ME, Masiarz FR, Valenzuela P, Truett M;

XX PI Favaloro J;

XX DR WPI; 2000-367967/32.

XX DR N-PSDB; AAA58444.

XX FT DNA sequence of portion of human Factor VIII C for treating and preventing
 XX FT the symptoms of hemophilia.
 XX PS Claim 3; Page 37; 39pp; English.
 XX CC The present sequence is the protein sequence for the 77/80kd subunit of
 CC human Factor VIII C. Factor VIII C is a plasma protein involved in blood
 CC coagulation, and is absent or defective in haemophilia A. The Factor
 CC VIII C protein can, therefore, be used to treat haemophilia, as well as in
 CC the production of monoclonal antibodies to Factor VIII C, and in

CC diagnostic assays for the presence of Factor VIII subunits in
 CC physiological fluids, for example blood or serum

XX SQ Sequence 73 AA;

Query Match 100.0%; Score 28; DB 3; Length 73;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYQMS 5

Db 60 DYQMS 64

|||||

RESULT 25

AAB40073

ID AAB40073 standard; protein; 98 AA.

XX AC AAB40073;

XX DT 05-FEB-2001 (first entry)

XX DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 599.

XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

XX OS Homo sapiens.

XX FN WO200056772-A1.

XX PD 28-SEP-2000.

XX PF 24-MAR-2000; 2000WO-US007946.

XX PR 25-MAR-1999; 99US-0126603P.

XX (BADI) BASF AG.

XX PA (GEMY) GENETICS INST INC.

XX PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 XX treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 XX disease and multiple sclerosis.

XX Claim 75; Page 121; 377pp; English.

XX This invention relates to a new human antibody specific for human
 XX interleukin-12 (IL-12). The invention also includes antigen binding
 XX portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 XX anti-IL-12 antibody heavy and light chain complementarity determining
 XX region (CDR) amino acid sequences, and also includes variable region
 XX amino acid sequences. Other variable region amino acid sequences are
 XX given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 XX represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 XX represent other CDR sequences. Light chain CDR3 consensus sequences are
 XX given in AAB40064-B40067. Primers used in the identification and
 XX construction of the antibodies of the invention are given in AAC61062-
 XX C61071. The antibody of the invention is a neutralising antibody and has
 XX antirheumatic; antiarthritic; antisclerotic; antinflammatory;
 XX neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
 XX antibacterial and immunosuppressive activity. The antibodies or antigen-
 XX binding fragments are useful in the treatment of disorders associated
 XX with detrimental release of human IL-12, especially Crohn's disease,

CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders

SQ Sequence 98 AA;

Query Match 100.0%; Score 28; DB 3; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 DYGMS 5
 |||||
 Db 31 DYGMS 35

RESULT 26

ABG78186
 ID ABG78186 standard; protein; 98 AA.

AC ABG78186;

XX 15-NOV-2002 (first entry)

DT Human Fv molecule hypervariable region related peptide #61.

DE Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
 KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
 KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

OS WO200259264-A2.

PN 01-AUG-2002.

PF 31-DEC-2001; 2001WO-US049440.

PR 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

PI Plakain D, Peretz T;

XX WPI; 2002-619166/66.

PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 or fragment, or construct of fragment with enhanced binding
 PT characteristics so as to selectively bind target cell in favor of other
 PT cells.

PS Claim 13; Page 177-178; 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention

XX Sequence 98 AA;

Query Match 100.0%; Score 28; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 |||||
 Db 31 DYGMS 35

RESULT 27

ABG91877
 ID ABG91877 standard; protein; 98 AA.

XX ABG91877;

DT 04-DEC-2002 (first entry)

DE Human antibody fragment #61.

XX Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW retastosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.

XX Homo sapiens.

OS WO200253700-A2.

PN 11-JUL-2002.

PF 31-DEC-2001; 2001WO-US049442.

PR 29-DEC-2000; 2000US-00751181.

PR 29-DEC-2000; 2000US-0258948P.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.

PT Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.

PS Disclosure; Page 255; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention

XX Sequence 98 AA;

Query Match 100.0%; Score 28; DB 5; Length 98;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 DYGMS 5
Db 31 DYGMS 35
|||||

RESULT 28
ABO27087
ID ABO27087 standard; protein; 98 AA.

XX AC ABO27087;
XX DT 10-SEP-2003 (first entry)
XX DE Human germline heavy chain variable region gene segment #20.
XX KW Human; heavy chain variable region; VH; humanised antibody;
XX KW chimeric antibody; complementarity determining region; CDR;
XX KW canonical CDR structure type.

XX OS Homo sapiens.

XX PN US2003039649-A1.

XX XX 27-FEB-2003.

XX XX 12-JUL-2002; 2002US-00194975.

XX PR 12-JUL-2001; 2001US-0305111P.

XX PA (FOOT/) FOOTE J.

XX PI Foote J;

XX DR WPI, 2003-492151/46.

XX Making humanized antibody for converting antibody, by making chimeric
XX antibodies containing complementarity determining region from non-human
XX antibody and appropriate framework sequences of human antibodies.

XX Example 1; Fig 1; 31pp; English.

XX The invention describes a method of making a humanised antibody,
XX comprising making chimeric antibodies containing a complementarity
XX determining region (CDR) from a non-human antibody and appropriate
XX framework sequences (I) of human antibodies. (I) is selected by using
XX canonical CDR structure types of non-human antibody in comparison to
XX germline canonical CDR structure types of human antibodies as the basis
XX for selection, for humanisation. The method is useful for making a
XX humanised antibody or a converted antibody. The method is applicable for
XX converting a subject antibody sequence of any subject species to a less
XX immunogenic form suitable for use in an object species. The method is
XX reliable for identifying suitable human framework sequences to support
XX non-human CDR regions and to provide humanised antibodies that retain
XX high antigen binding with low immunogenicity in humans, without the need
XX for direct comparison of framework sequences, without the need for
XX determining critically important amino acid residues in the framework,
XX and without the need for multiple iteration and construction to obtain
XX humanised antibodies with suitable therapeutic properties. The antibody
XX has high affinity and low immunogenicity without need for comparing
XX framework sequences between non-human and human antibodies. This sequence
XX represents a human heavy chain variable region gene segment used in the
XX creation of humanised antibodies

XX Sequence 98 AA;

Query Match 100.0%; Score 28; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 31 DYGMS 35
|||||

RESULT 29
ADF09916
ID ADF09916 standard; protein; 98 AA.

XX AC ADF09916;

XX DT 12-FEB-2004 (first entry)

XX DE Antibody heavy chain variable region VH_3-20.

XX KW Antibody; stability; solubility; antigen binding affinity;
XX KW variable region; human.

XX OS Homo sapiens.

XX PN WO2003074679-A2.

XX PD 12-SEP-2003.

XX PF 03-MAR-2003; 2003WO-US006598.

XX PR 01-MAR-2002; 2002US-0360843P.

XX PR 29-MAY-2002; 2002US-0384197P.

XX PA (XENC-) XENCOR.

XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX DR WPI, 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
XX comprises analyzing the interactions of amino acids at variable
XX positions.

XX Disclosure; Fig 2a; 135pp; English.

XX The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.

XX Sequence 98 AA;

Query Match 100.0%; Score 28; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

Db 31 DYGMS 35
|||||

RESULT 30
ADF10126
ID ADF10126 standard; protein; 98 AA.

XX AC ADF10126;

XX DT 12-FEB-2004 (first entry)

```
XX DE Antibody heavy chain variable region VH_3-20.
XX KW Antibody; stability; solubility; antigen binding affinity;
XX KW variable region; human.
XX OS Homo sapiens.
XX FN WO2003074679-A2.
XX PD 12-SEP-2003.
XX PF 03-MAR-2003; 2003WO-US006598.
XX PR 01-MAR-2002; 2002US-0360843P.
XX PR 29-MAY-2002; 2002US-0384197P.
XX PA (XENC-) XENCOR.
XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX WIPI; 2003-722066/68.
XX CC Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX PS Example 16; Fig 40a; 135pp; English.
XX CC The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX SQ Sequence 98 AA;
XX Query Match 100.0%; Score 28; DB 7; Length 98;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DYGMS 5
XX DB 31 DYGMS 35
XX RESULT 31
XX ADF10024
XX ID ADF10024 standard; protein; 98 AA.
XX AC ADF10024;
XX DT 12-FEB-2004 (first entry)
XX DE VEGF antibody heavy chain variable region VH_3-20.
XX KW Antibody; stability; solubility; antigen binding affinity;
XX KW variable region; human; VEGF.
XX OS Homo sapiens.
XX FN WO2003074679-A2.
XX PD 12-SEP-2003.
XX PF 03-MAR-2003; 2003WO-US006598.
XX PR 01-MAR-2002; 2002US-0360843P.
XX PR 29-MAY-2002; 2002US-0384197P.
XX PA (XENC-) XENCOR.
XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX WIPI; 2003-722066/68.
XX CC Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX PS Example 16; Fig 40a; 135pp; English.
XX CC The present invention relates to a method for optimizing at least one
XX physico-chemical property of an antibody by a computational screening
XX method. The method comprises: receiving a template antibody structure;
XX selecting at least one variable position belonging to the antibody
XX structure; selecting at least one amino acid to be considered at the
XX variable position(s); analyzing the interaction of each selected amino
XX acid at each variable position with at least part of the remainder of the
XX antibody, including the selected amino acids at other variable positions;
XX and identifying a set of at least one antibody sequence with at least one
XX optimized physico-chemical property. The method is useful for optimizing
XX the physico-chemical properties of an antibody, especially the stability,
XX solubility, or antigen binding affinity. The optimized antibody may be
XX useful for treating a patient. The present sequence is an antibody
XX variable region sequence used to illustrate the invention.
XX SQ Sequence 98 AA;
XX Query Match 100.0%; Score 28; DB 7; Length 98;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 DYGMS 5
XX DB 31 DYGMS 35
XX RESULT 32
XX ADJ80300
XX ID ADJ80300 standard; protein; 98 AA.
XX AC ADJ80300;
XX DT 06-MAY-2004 (first entry)
XX DE VH gene locus antibody amino acid sequence #20.
XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.
XX OS Homo sapiens.
XX FN WO2003048321-A2.
XX PD 12-JUN-2003.
XX PF 03-DEC-2002; 2002WO-US038450.
XX PR 03-DEC-2001; 2001US-0336591P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Rother R, Wu D;
XX WIPI; 2003-513753/48.
XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively
```

PT linking the selected framework sequences to one or more complementarity
PT determining regions of the initial antibody.
XX
PS Disclosure; SEQ ID NO 60; 77pp; English.
XX
XX The invention relates to a method of producing a hybrid antibody or
CC hybrid antibody fragment by: (i) providing an initial antibody having
CC specificity for a target; (ii) determining the sequence of a variable
CC region of the initial antibody; (iii) selecting a first component of the
CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
CC sequence of the first component to sequences contained in a reference
CC database of antibody sequences or antibody fragment sequences from a
CC target species; (v) selecting a sequence from an antibody in the database
CC which demonstrates a high degree of homology to the first component; (vi)
CC selecting a second component of the variable region which is different
CC than the first component, the second component selected from the group
CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
CC second component to sequences contained in a reference database of
CC antibody sequences or antibody fragment sequences from the target species
CC; (viii) selecting a sequence from the database which demonstrates a high
CC degree of homology to the second component and which is from a different
CC antibody than the selected antibody; and (ix) operatively linking the
CC selected framework sequences to one or more complementarity determining
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC hybrid antibody fragment. The method is useful for producing a hybrid
CC antibody or hybrid antibody fragment (claimed). The antibody and
CC fragments are useful for therapeutic and diagnostic purposes. The method
CC uses entire framework regions from a single antibody variable heavy or
CC variable light chain to receive the CDRs. This produces antibodies that
CC are highly homologous and exhibit reduced immunogenicity while
CC maintaining an optimum binding profile. This sequence represents the
CC amino acid sequence of an antibody from the VH gene locus.
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 28; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 31 DYGMS 35
RESULT 33
ADY75305
ID ADY75305 standard; protein; 98 AA.
XX
AC ADY75305;
XX
XX 02-JUN-2005 (first entry)
DT
DE Protein encoded by human germline heavy chain V minigene VH3 3-20.
XX
XX Antibody engineering; antibody; antibody production; gene library;
KW DNA recombination; gene amplification; primer extension;
KW heavy chain variable region.
XX
OS Homo sapiens.
XX
XX WO2005023993-A2.
PN
XX 17-MAR-2005.
FD
XX 09-SEP-2004; 2004WO-US029617.
PP
XX 09-SEP-2003; 2003US-0501073P.
PR
XX (INTE-) INTEGRIGEN INC.
PA
XX Sharma V, Leonard L, Smider V;
PI
XX WPI, 2005-223364/23.
DR

XX
PT Producing polynucleotide encoding human germline antibody V-region for
PT generating full-length antibody germline V-region genes, by obtaining v
PT or J minigene and joining V minigene with J minigene, or joining J
PT minigene with V minigene.
XX
PS Disclosure; Fig 10; 52pp; English.
XX
XX The present invention relates to producing germline antibody genes by a
CC completely in vitro approach that mimics the natural process of V(D)J
CC recombination. The antibody genes are completely human and native in
CC their sequence, and libraries of such antibody genes can be constructed
CC which represent an unselected population representing the entire antibody
CC repertoire. The method uses gene amplification to produce a V minigene, a D
CC and a hybrid primer capable of hybridizing to a V minigene and either a D
CC or V minigene. The hybrid primer facilitates recombination of a V
CC minigene to a D or J minigene to produce a full length V-region gene.
CC Also disclosed is a library comprising member polynucleotides encoding a
CC exogenously rearranged human germline antibody V-regions. In producing a
CC polynucleotide encoding a human germline antibody V-region, a D minigene
CC is further joined to the 3' end of the V minigene and the 5' end of the J
CC minigene. The V minigene or the J minigene in is obtained by chemical
CC synthesis or by amplification from a germline DNA library. Joining the V
CC minigene with at least one J minigene is performed by primer extension
CC using at least two or three oligonucleotide primers. The V minigene is
CC derived from human immunoglobulin kappa locus, human immunoglobulin
CC lambda locus, or human immunoglobulin heavy chain locus. The V-region
CC also comprises a serine protease triad. The human germline antibodies can
CC be used as precursors to more high affinity antibodies, and are useful in
CC the generation of efficiently pairing libraries of heavy and light
CC chains. The present sequence is a polypeptide encoded by human germline
CC heavy chain V minigene, family VH3 locus 3-20.
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 28; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 31 DYGMS 35
RESULT 34
AA95177
ID AA95177 standard; protein; 113 AA.
XX
AC AA95177;
XX
XX 29-AUG-2000 (first entry)
DT
DE Anti-platelet glycoprotein Ib human HIB-1 VH.
XX
XX Variable heavy chain; single chain antibody; scFv; human; HIB-1;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH Key 1..30
FT Region /note= "framework region 1"
FT Region 31..34
FT Region /note= "complementarity determining region 1"
FT Region 35..49
FT Region /note= "framework region 2"
FT Region 50..66
FT Region /note= "complementarity determining region 2"
FT Region 67..98
FT Region /note= "framework region 3"
FT Region 99..104
FT Region /note= "complementarity determining region 3"

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FT Region 105. .113
FT /note= "framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US025495.
XX 30-OCT-1998; 98US-0106275P.
XX (MILL/) MILLER J L.
XX Miller JL;
XX WPI; 2000-365744/31.
XX N-PSDB; AAA27658.
XX
XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
XX Ib alpha molecule useful for producing antibodies which inhibit platelet
XX aggregation.
XX Claim 10; Page 71; 89pp; English.
XX
XX The present sequence is that of the heavy chain variable region (VH) of
XX human single chain antibody (scFv) Hib-1 (see AAY95198), which is
XX directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv
XX was isolated from a human synthetic VH and VL scFv library by 3 rounds of
XX phagmid selection against transfected CHO cells expressing the GPIb
XX alpha component of the GPIb/IX/V complex on their surface, followed by a
XX 4th round of selection against washed human platelets, and 2 final rounds
XX in which attempts were made to displace scFv from washed platelets by
XX flooding with murine monoclonal antibody or mimotope peptide (see
XX AAY95229). Whether displayed as surface proteins on a phagemid or
XX secreted as free scFv by Escherichia coli, the Hib scFv clones are
XX capable of inhibiting von Willebrand factor-dependent aggregation of
XX platelets. The scFv are composed of native human protein sequences and
XX are therefore attractive potential reagents for therapeutic purposes.
XX They provide a new class of antithrombotic agents, useful for the
XX prevention of platelet-dependent thrombi in diseased arteries, bypass
XX grafts, dialysis etc., and can also be used as diagnostic reagents.
XX Methods of inhibiting aggregation of platelets, of binding human platelet
XX GPIb alpha and of selecting a VH or VL region of an antibody that
XX inhibits platelet aggregation are claimed. Note: The present sequence is
XX not shown in the specification but is derived from the Hib-1 VH sequence
XX given on page 71 (see AAY95177)
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 28; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 31 DYGMS 35

RESULT 35
AAY95178
ID AAY95178 standard; protein; 113 AA.
XX
XX AAY95178;
XX
XX 29-AUG-2000 (first entry)
XX
XX Anti-platelet glycoprotein Ib human Hib-1 VH.
XX
XX Variable heavy chain; single chain antibody; scFv; human; Hib-1;
XX glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX antithrombotic; thrombus; therapy; diagnostic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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FT Region 1. .30
FT /note= "framework region 1"
XX 31. .34
XX /note= "complementarity determining region 1"
XX 35. .49
XX /note= "framework region 2"
XX 50. .66
XX /note= "complementarity determining region 2"
XX 67. .98
XX /note= "framework region 3"
XX 99. .104
XX /note= "complementarity determining region 3"
XX 105. .113
XX /note= "framework region 4"
XX
XX WO200026667-A1.
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025495.
XX 30-OCT-1998; 98US-0106275P.
XX (MILL/) MILLER J L.
XX Miller JL;
XX WPI; 2000-365744/31.
XX
XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
XX Ib alpha molecule useful for producing antibodies which inhibit platelet
XX aggregation.
XX Claim 10; Page; 89pp; English.
XX
XX The present sequence is that of the heavy chain variable region (VH) of
XX human single chain antibody (scFv) Hib-1 (see AAY95198), which is
XX directed against platelet glycoprotein Ib (GPIb). The Hib series of scFv
XX was isolated from a human synthetic VH and VL scFv library by 3 rounds of
XX phagmid selection against transfected CHO cells expressing the GPIb
XX alpha component of the GPIb/IX/V complex on their surface, followed by a
XX 4th round of selection against washed human platelets, and 2 final rounds
XX in which attempts were made to displace scFv from washed platelets by
XX flooding with murine monoclonal antibody or mimotope peptide (see
XX AAY95229). Whether displayed as surface proteins on a phagemid or
XX secreted as free scFv by Escherichia coli, the Hib scFv clones are
XX capable of inhibiting von Willebrand factor-dependent aggregation of
XX platelets. The scFv are composed of native human protein sequences and
XX are therefore attractive potential reagents for therapeutic purposes.
XX They provide a new class of antithrombotic agents, useful for the
XX prevention of platelet-dependent thrombi in diseased arteries, bypass
XX grafts, dialysis etc., and can also be used as diagnostic reagents.
XX Methods of inhibiting aggregation of platelets, of binding human platelet
XX GPIb alpha and of selecting a VH or VL region of an antibody that
XX inhibits platelet aggregation are claimed. Note: The present sequence is
XX not shown in the specification but is derived from the Hib-1 VH sequence
XX given on page 71 (see AAY95177)
XX
SQ Sequence 113 AA;
Query Match 100.0%; Score 28; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 31 DYGMS 35

RESULT 36
AAY95189
ID AAY95189 standard; protein; 115 AA.
XX

```

AC AAY95189;

XX 29-AUG-2000 (first entry)

XX Anti-platelet glycoprotein Ib human HIB-1 VH.

XX

XX Variable heavy chain; single chain antibody; scFv; human; HIB-1;

XX glycoprotein Ib alpha; platelet; aggregation; antiaggregant;

XX antithrombotic; thrombus; therapy; diagnostic.

XX

OS Homo sapiens.

XX

XX Location/Qualifiers

FT 1..30

FT Region

FT /note= "framework region 1"

FT Region

FT 31..34

FT /note= "complementarity determining region 1"

FT Region

FT 35..49

FT /note= "framework region 2"

FT Region

FT 50..66

FT /note= "complementarity determining region 2"

FT Region

FT 67..98

FT /note= "framework region 3"

FT Region

FT 99..104

FT /note= "complementarity determining region 3"

FT Region

FT 105..115

FT /note= "framework region 4"

XX

PN WO200026667-A1.

XX

PD 11-MAY-2000.

XX

PF 29-OCT-1999; 99WO-US025495.

XX

PR 30-OCT-1998; 98US-0106275P.

XX

XX (MILL/) MILLER J L.

PA

PI Miller JL;

XX

XX MPI, 2000-365744/31.

XX

XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

XX Ib alpha molecule useful for producing antibodies which inhibit platelet

XX aggregation.

XX

XX Claim 13; Fig 5; 89pp; English.

XX

XX The present sequence is that of the heavy chain variable region (VH) of

XX human single chain antibody (scFv) HIB-1 (see AAY95190), which is

XX directed against platelet glycoprotein Ib (GPIb). The HIB series of scFv

XX was isolated from a human synthetic VH and VL scFv library by 3 rounds of

XX phagemid selection against transfected CHO cells expressing the GPIb

XX alpha component of the GPIb/IX/V complex on their surface, followed by a

XX 4th round of selection against washed human platelets, and 2 final rounds

XX in which attempts were made to displace scFv from washed platelets by

XX flooding with murine monoclonal antibody or mimotope peptide (see

XX AAY95229). Whether displayed as surface proteins on a phagemid or

XX secreted as free scFv by Escherichia coli, the HIB scFv clones are

XX capable of inhibiting von Willebrand factor-dependent aggregation of

XX platelets. The scFv are composed of native human protein sequences and

XX are therefore attractive potential reagents for therapeutic purposes.

XX They provide a new class of antithrombotic agents, useful for the

XX prevention of platelet-dependent thrombi in diseased arteries, bypass

XX grafts, dialysis etc., and can also be used as diagnostic reagents.

XX Methods of inhibiting aggregation of platelets, of binding human platelet

XX GPIb alpha and of selecting a VH or VL region of an antibody that

XX inhibits platelet aggregation are claimed

XX

SQ Sequence 115 AA;

Query Match 100.0%; Score 28; DB 3; Length 115;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5

Db 31 DYGMS 35

RESULT 37

AAY95190

ID AAY95190 standard; protein; 115 AA.

XX

XX AAY95190;

XX

XX 29-AUG-2000 (first entry)

XX Anti-platelet glycoprotein Ib human HIB-1 VH.

XX

XX Variable heavy chain; single chain antibody; scFv; human; HIB-1;

XX glycoprotein Ib alpha; platelet; aggregation; antiaggregant;

XX antithrombotic; thrombus; therapy; diagnostic.

XX

XX Homo sapiens.

XX

XX Location/Qualifiers

FT 1..30

FT Region

FT /note= "framework region 1"

FT Region

FT 31..34

FT /note= "complementarity determining region 1"

FT Region

FT 35..49

FT /note= "framework region 2"

FT Region

FT 50..66

FT /note= "complementarity determining region 2"

FT Region

FT 67..98

FT /note= "framework region 3"

FT Region

FT 99..104

FT /note= "complementarity determining region 3"

FT Region

FT 105..115

FT /note= "framework region 4"

XX

PN WO200026667-A1.

XX

PD 11-MAY-2000.

XX

PF 29-OCT-1999; 99WO-US025495.

XX

PR 30-OCT-1998; 98US-0106275P.

XX

XX (MILL/) MILLER J L.

PA

PI Miller JL;

XX

XX MPI, 2000-365744/31.

XX

XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

XX Ib alpha molecule useful for producing antibodies which inhibit platelet

XX aggregation.

XX

XX Claim 13; Page; 89pp; English.

XX

XX The present sequence is that of the heavy chain variable region (VH) of

XX human single chain antibody (scFv) HIB-1 (see AAY95190), which is

XX directed against platelet glycoprotein Ib (GPIb). The HIB series of scFv

XX was isolated from a human synthetic VH and VL scFv library by 3 rounds of

XX phagemid selection against transfected CHO cells expressing the GPIb

XX alpha component of the GPIb/IX/V complex on their surface, followed by a

XX 4th round of selection against washed human platelets, and 2 final rounds

XX in which attempts were made to displace scFv from washed platelets by

XX flooding with murine monoclonal antibody or mimotope peptide (see

XX AAY95229). Whether displayed as surface proteins on a phagemid or

XX secreted as free scFv by Escherichia coli, the HIB scFv clones are

XX capable of inhibiting von Willebrand factor-dependent aggregation of

XX platelets. The scFv are composed of native human protein sequences and

XX are therefore attractive potential reagents for therapeutic purposes.

XX They provide a new class of antithrombotic agents, useful for the

XX prevention of platelet-dependent thrombi in diseased arteries, bypass

XX grafts, dialysis etc., and can also be used as diagnostic reagents.

XX Methods of inhibiting aggregation of platelets, of binding human platelet

XX GPIb alpha and of selecting a VH or VL region of an antibody that

XX inhibits platelet aggregation are claimed

XX

SQ Sequence 115 AA;

Query Match 100.0%; Score 28; DB 3; Length 115;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents,
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIb alpha and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Note: The present sequence is
 CC not shown in the specification but is derived from the H1b-1 VH sequence
 CC given in Fig 5 (see AAY95189)

XX Sequence 115 AA;

Query Match 100.0%; Score 28; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||

Db 31 DYGMS 35

RESULT 38

AAW19880
 ID AAW19880 standard; protein; 116 AA.

AC AAW19880;

DT 07-DEC-1997 (first entry)

DE CEA-specific antibody CEA5 VH sequence.

XX Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
 KW lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1
 /note= "complementarity determining region 1"

FT Region 50..66

FT /label= CDR2
 /note= "complementarity determining region 2"

FT Region 99..105

FT /label= CDR3
 /note= "complementarity determining region 3"

FT WO720932-A1.

PN 12-JUN-1997.

PD 09-DEC-1996; 96WO-GB03043.

XX 07-DEC-1995; 95GB-00025004.

PR 23-MAY-1996; 96GB-00010824.

PR 11-OCT-1996; 96GB-00021295.

XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Osbourn JK, Allen DJ, McCafferty JG;

XX WPI; 1997-319779/29.

DR N-PSDB; AAT72130.

XX Specific binding members for human carcinoembryonic antigen - bind to the

PT A3-B3 extracellular domain of hCEA and are substantially non-cross-

PT reactive with human liver cells; used for diagnosing cancer.

XX Claim 7; Fig 1a; 128pp; English.

PS This polypeptide sequence comprises the heavy chain variable region (VH)

CC of human carcinoembryonic antigen (hCEA)-specific antibody CEA5. VH

CC (AAT72126-32) and VL (AAT72133-35) gene sequences were obtained for anti-

CC hCEA antibodies CEA1-CEA7 (see AAW19876-85). A claimed specific binding

CC member (A) comprises an hCEA specific antibody antigen binding domain
 CC that has a dissociation constant for hCEA of less than 1 x 10⁻⁸ M, is
 CC non-cross-reactive with human liver cells, and preferentially binds to
 CC the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA
 CC over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL
 CC sequences from CEA1-7, or their CDR sequences, as well as CEA6 VH and VL
 CC variants. (A) is used to detect cells expressing hCEA, in vivo or in
 CC vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma
 CC of the colon, lung or breast

XX Sequence 116 AA;

Query Match 100.0%; Score 28; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 |||||

Db 31 DYGMS 35

RESULT 39

AAR66312
 ID AAR66312 standard; protein; 117 AA.

AC AAR66312;

DT 25-MAR-2003 (revised)

DT 03-AUG-1995 (first entry)

XX Human immunoglobulin variable heavy chain #18.

XX Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.

XX Homo sapiens.

XX WO9426895-A1.

XX 24-NOV-1994.

XX 10-MAY-1993; 93WO-JP000603.

XX 10-MAY-1993; 93WO-JP000603.

XX (NISR) JAPAN TOBACCO INC.

XX Honjo T, Matsuda F;

XX WPI; 1995-006791/01.

XX N-PSDB; AAR78958.

XX DNA fragment comprising human immunoglobulin Vh genes - for the

XX production of human immunoglobulin in mammalian hosts.

XX Claim 29; Page 56-57; 130pp; Japanese.

XX Protein sequences (AAR66295-51) are novel human immunoglobulin heavy

XX chain sequences encoded by novel isolated genes. The genes (AAQ78939-

XX 79002) were isolated and cloned from a series of cosmid constructs: Y202;

XX Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using

XX primers AAQ78917-38. The genes are subdivided into 5 families of Vh

XX genes. The fragments cover a region of 800 kb. The DNA fragments were

XX isolated from high molecular weight DNA from human placenta. The DNA was

XX partially digested with RsaI restriction enzyme. The fragments were

XX separated by gel electrophoresis and 35-45 kb fractions were collected.

XX The fragments were ligated with ClaI-digested cosmid vector pJB81. The

XX ligation products were in vitro packaged and infected into E.coli 490A. The

XX fragments were then subcloned by colony hybridisation. The Vh genes and

XX the DNA fragments encoding them are useful in producing human

XX immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN

XX field.)

SQ Sequence 117 AA;
Query Match 100.0%; Score 28; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYGMS 5
|
|
|
|
|
DB 50 DYGMS 54

RESULT 40
ADX01783
ID ADX01783 standard; protein; 117 AA.
XX AC ADX01783;
XX DT 21-APR-2005 (first entry)
XX DE SARS coronavirus antibody heavy chain SEQ ID NO 39.
XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX KW respiratory disease; infection; antibody; heavy chain.
XX OS SARS coronavirus.
XX PN WO2005012360-A2.
XX PD 10-FEB-2005.
XX PF 21-JUL-2004; 2004WO-EP051568.
XX PR 22-JUL-2003; 2003WO-EP050328.
XX PR 01-SEP-2003; 2003WO-EP050391.
XX PR 16-OCT-2003; 2003WO-EP050723.
XX PR 24-NOV-2003; 2003WO-EP050883.
XX PR 04-DEC-2003; 2003WO-EP050943.
XX PR 02-FEB-2004; 2004WO-EP050067.
XX PR 13-FEB-2004; 2004WO-EP050127.
XX PR 19-MAR-2004; 2004WO-EP050334.
XX PR 07-APR-2004; 2004WO-EP050464.
XX PR 14-APR-2004; 2004WO-EP050516.
XX PR 29-APR-2004; 2004WO-EP050643.
XX PA (CRUC-) CRUCCELL HOLLAND BV.
XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
XX DR WPI; 2005-142879/15.
XX DR N-PSDB; ADX01782.
XX PT New binding molecules that specifically bind to severe acute respiratory
XX PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
XX PT treating conditions resulting from SARS-CoV.
XX PS Claim 4; SEQ ID NO 39; 633pp; English.
XX CC The invention relates to a binding molecule, or its variant, capable of
XX CC specifically binding to a severe acute respiratory syndrome (SARS)-
XX CC coronavirus (CoV). The composition (including the binding molecule or its
XX CC functional variant, or the immunoconjugate) is useful as a medicament for
XX CC the diagnosis, prophylaxis or treatment of a condition resulting from a
XX CC SARS-CoV, or in the preparation of the medicament. The present sequence
XX CC represents a SARS coronavirus binding molecule heavy chain.
SQ Sequence 117 AA;
Query Match 100.0%; Score 28; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYGMS 5
|
|
|
|
|

Db 33 DYGMS 37
Search completed: November 18, 2005, 21:08:11
Job time : 68.9286 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:02:00 ; Search time 15.8929 Seconds
(without alignments)
26.010 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28

Sequence: 1 DYGM5 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/PCRTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	16	1	US-08-480-190-170 Sequence 170, App
2	28	100.0	16	1	US-08-488-379-170 Sequence 170, App
3	28	100.0	16	2	US-08-475-399A-170 Sequence 170, App
4	28	100.0	16	2	US-08-077-255A-170 Sequence 170, App
5	28	100.0	16	2	PCT-US93-07545-170 Sequence 170, App
6	28	100.0	98	2	US-10-194-975-20 Sequence 20, Appl
7	28	100.0	98	2	US-09-534-717-599 Sequence 599, App
8	28	100.0	116	1	US-08-652-816A-14 Sequence 14, Appl
9	28	100.0	117	2	US-08-545-809A-106 Sequence 106, App
10	28	100.0	117	2	US-09-515-697-105 Sequence 106, App
11	28	100.0	232	2	US-09-489-039A-8586 Sequence 8586, App
12	28	100.0	258	2	US-09-107-532A-4002 Sequence 4002, Ap
13	28	100.0	264	2	US-09-107-532A-6813 Sequence 6813, Ap
14	28	100.0	309	2	US-09-079-029-9 Sequence 9, Appli
15	28	100.0	354	2	US-08-724-984A-2 Sequence 2, Appli
16	28	100.0	373	2	US-09-828-995B-35 Sequence 35, Appl
17	28	100.0	470	2	US-09-828-995B-11 Sequence 11, Appl
18	28	100.0	474	2	US-09-486-192-4 Sequence 4, Appli
19	28	100.0	474	2	US-10-328-459A-4 Sequence 4, Appli
20	28	100.0	520	2	US-09-502-540-11365 Sequence 11365, A
21	28	100.0	868	1	US-07-864-004B-6 Sequence 6, Appli
22	28	100.0	868	1	US-08-251-937A-6 Sequence 3, Appli
23	28	100.0	868	1	US-08-212-133A-3 Sequence 3, Appli
24	28	100.0	1090	4	PCT-US93-03275-6 Sequence 6, Appli
25	28	100.0	1438	2	US-09-209-916-1 Sequence 1, Appli
26	28	100.0	1443	1	US-08-670-707A-39 Sequence 39, Appl
27	28	100.0	1443	2	US-09-037-601-39 Sequence 39, Appl

28	28	100.0	1443	2	US-09-315-179-39	Sequence 39, Appl
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30	28	100.0	1447	2	US-09-407-605-4	Sequence 4, Appli
31	28	100.0	1457	2	US-09-001-039B-47	Sequence 47, Appl
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34	28	100.0	1661	1	US-08-882-083-2	Sequence 2, Appli
35	28	100.0	1661	1	US-08-558-107-2	Sequence 2, Appli
36	28	100.0	1661	2	US-09-243-539-2	Sequence 5, Appli
37	28	100.0	2115	2	US-09-324-867-5	Sequence 37, Appl
38	28	100.0	2133	1	US-08-670-707A-37	Sequence 37, Appl
39	28	100.0	2133	2	US-09-037-601-37	Sequence 37, Appl
40	28	100.0	2133	2	US-09-315-179-37	Sequence 37, Appl
41	28	100.0	2133	2	US-09-523-656-30	Sequence 30, Appl
42	28	100.0	2304	2	US-09-324-867-4	Sequence 4, Appli
43	28	100.0	2319	1	US-08-212-133A-8	Sequence 8, Appli
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48	28	100.0	2319	2	US-09-523-656-28	Sequence 28, Appl
49	28	100.0	2319	4	PCT-US94-13200-6	Sequence 6, Appli
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60	28	100.0	2332	2	US-09-957-641A-2	Sequence 2, Appli
61	28	100.0	2332	2	US-10-360-101-229	Sequence 229, App
62	28	100.0	2332	4	PCT-US93-03275-4	Sequence 4, Appli
63	28	100.0	2332	4	PCT-US94-13200-2	Sequence 2, Appli
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65	28	100.0	2351	1	US-08-121-202-2	Sequence 2, Appli
66	28	100.0	2351	1	US-08-366-851A-2	Sequence 2, Appli
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68	28	100.0	2351	2	US-09-001-039B-45	Sequence 45, Appl
69	28	100.0	2351	6	5171844-2	Patent No. 5171844
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71	25	89.3	5	2	US-08-836-561-34	Sequence 34, Appl
72	25	89.3	5	2	US-09-434-122-34	Sequence 34, Appl
73	25	89.3	97	2	US-09-489-039A-8140	Sequence 8140, Ap
74	25	89.3	97	2	US-09-270-767-38591	Sequence 38591, A
75	25	89.3	97	2	US-09-270-767-53808	Sequence 53808, A
76	25	89.3	113	2	US-09-905-223-439	Sequence 439, App
77	25	89.3	121	2	US-09-489-039A-10860	Sequence 10860, A
78	25	89.3	140	2	US-08-836-561-23	Sequence 23, Appl
79	25	89.3	140	2	US-09-434-122-23	Sequence 23, Appl
80	25	89.3	143	2	US-09-543-681A-7784	Sequence 7784, Ap
81	25	89.3	143	2	US-09-424-978B-20	Sequence 20, Appl
82	25	89.3	197	2	US-10-101-464A-502	Sequence 502, App
83	25	89.3	215	2	US-09-270-767-61999	Sequence 61999, A
84	25	89.3	228	2	US-09-198-452A-849	Sequence 849, App
85	25	89.3	230	2	US-09-485-737B-102	Sequence 102, App
86	25	89.3	230	2	US-10-071-485-102	Sequence 102, App
87	25	89.3	235	2	US-09-485-737B-93	Sequence 93, Appl
88	25	89.3	235	2	US-10-071-485-93	Sequence 93, Appl
89	25	89.3	240	2	US-09-485-737B-91	Sequence 91, Appl
90	25	89.3	240	2	US-09-820-155-26	Sequence 26, Appl
91	25	89.3	240	2	US-10-071-485-91	Sequence 91, Appl
92	25	89.3	265	2	US-09-270-767-46420	Sequence 46420, A
93	25	89.3	267	2	US-09-485-737B-2	Sequence 2, Appli
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95	25	89.3	269	2	US-09-107-532A-6557	Sequence 6557, Ap
96	25	89.3	294	2	US-09-489-039A-8975	Sequence 8975, Ap
97	25	89.3	304	2	US-09-328-352-7289	Sequence 7289, Ap
98	25	89.3	305	2	US-08-858-207A-408	Sequence 408, App
99	25	89.3	324	2	US-10-126-279-17	Sequence 17, Appl
100	25	89.3	324	2	US-10-286-606-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-480-190-170
; Sequence 170, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-170

Query Match 100.0%; Score 28; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 3 DYGMS 7
RESULT 2
US-08-488-379-170
; Sequence 170, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-170

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Best Local Similarity 100.0%; Pred. No. 4.7;
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Db 3 DYGMS 7
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US-08-475-399A-170
; Sequence 170, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 3 DYGMS 7
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US-08-475-399A-170
; Sequence 170, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 3 DYGMS 7
RESULT 3
US-08-475-399A-170
; Sequence 170, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 3 DYGMS 7
RESULT 3
US-08-475-399A-170
; Sequence 170, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-170

Query Match 100.0%; Score 28; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 3 DYGMS 7

RESULT 4

US-08-077-255A-170
Sequence 170, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

TELEX: 200154
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-170

Query Match 100.0%; Score 28; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 3 DYGMS 7

RESULT 5

PCT-US93-07545-170
Sequence 170, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-170

Query Match 100.0%; Score 28; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 3 DYGMS 7

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RESULT 6
US-10-194-975-20
; Sequence 20, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-20

Query Match          100.0%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 7
US-09-534-717-599
; Sequence 599, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-599

Query Match          100.0%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 8
US-08-652-816A-14
; Sequence 14, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

Query Match          100.0%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 9
US-08-545-809A-106
; Sequence 106, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
```

```
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-652-816A-14

Query Match          100.0%; Score 28; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 9
US-08-545-809A-106
; Sequence 106, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
```

; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-106

Query Match 100.0%; Score 28; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 50 DYGMS 54

RESULT 10
US-09-515-697-106
; Sequence 106, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-Feb-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-515-697-106

Query Match 100.0%; Score 28; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 50 DYGMS 54

RESULT 11
US-09-489-039A-8586
; Sequence 8586, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8586
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8586

Query Match 100.0%; Score 28; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 219 DYGMS 223

RESULT 12
US-09-107-532A-4002
; Sequence 4002, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lytn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4002:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...258
; SEQUENCE DESCRIPTION: SEQ ID NO: 4002:
US-09-107-532A-4002

Query Match 100.0%; Score 28; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 172 DYGMS 176

RESULT 13
US-09-107-532A-6813
; Sequence 6813, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6813:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...264
; SEQUENCE DESCRIPTION: SEQ ID NO: 6813:
US-09-107-532A-6813

Query Match 100.0%; Score 28; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 70 DYGMS 74

RESULT 14
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-9

Query Match 100.0%; Score 28; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 70 DYGMS 74
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RESULT 15
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CKR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2

Query Match 100.0%; Score 28; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 15 DYGMS 19

RESULT 16
US-09-828-995B-35
; Sequence 35, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Canis familiaris

US-08-724-984A-2

Query Match 100.0%; Score 28; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 15 DYGMS 19

RESULT 16
US-09-828-995B-35
; Sequence 35, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Canis familiaris

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US-09-828-995B-35

Query Match 100.0%; Score 28; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 50 DYGMS 54

RESULT 17
US-09-828-995B-11
; Sequence 11, Application US/09828995B
; Patent No. 6703360
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/09/828,995B
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-828-995B-11

Query Match 100.0%; Score 28; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 50 DYGMS 54

RESULT 18
US-09-486-192-4
; Sequence 4, Application US/09486192
; Patent No. 6521440
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC386-US
; CURRENT APPLICATION NUMBER: US/09/486,192
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US98/18677
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: EP9719637.2
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Schizocaccaromyces pombe
US-09-486-192-4

Query Match 100.0%; Score 28; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 349 DYGMS 353

```

RESULT 19
US-10-328-459A-4
; Sequence 4, Application US/10328459A
; Patent No. 6905868
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC386-PCT
; CURRENT APPLICATION NUMBER: US/10/328,459A
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/
; PRIOR FILING DATE: 1997-09-15
; PRIOR APPLICATION NUMBER: EP9719637.2
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-328-459A-4

Query Match 100.0%; Score 28; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 349 DYGMS 353

RESULT 20
US-09-902-540-11365
; Sequence 11365, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11365
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11365

Query Match 100.0%; Score 28; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 389 DYGMS 393

RESULT 21
US-07-864-004B-6
; Sequence 6, Application US/07864004B
; Patent No. 5364771
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marshall S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,004B
; FILING DATE: 07 APRIL 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabet, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
US-07-864-004B-6

Query Match 100.0%; Score 28; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 804 DYGMS 808

RESULT 22
US-08-251-937A-6
; Sequence 6, Application US/08251937A
; Patent No. 5583209
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marshall S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/251,937A
; FILING DATE: 31-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004

; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pratt, John S.
; REGISTRATION NUMBER: 29,476
; REFERENCE/DOCKET NUMBER: EMU106DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6367
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
; US-08-251-937A-6

Query Match 100.0%; Score 28; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 804 DYGMS 808

RESULT 23

US-08-212-133A-3
; Sequence 3, Application US/08212133A
; Patent No. 5663060
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marschall S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212.133A
; FILING DATE: March 11, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU/76677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..868
; OTHER INFORMATION: /note= "Predicted amino acid
; sequence of the B and part of the A2 domains of
; OTHER INFORMATION: porcine factor VIII."
; US-08-212-133A-3

Query Match 100.0%; Score 28; DB 1; Length 868;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 804 DYGMS 808

RESULT 24

PCT-US93-03275-6
; Sequence 6, Application PC/TUS9303275
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marschall S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-4530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03275
; FILING DATE: 19930407
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU 106PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1090 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
; PCT-US93-03275-6

Query Match 100.0%; Score 28; DB 4; Length 1090;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DYGMS 5
      |||||
Db      1026 DYGMS 1030

RESULT 25
US-09-209-916-1
; Sequence 1, Application US/09209916
; Patent No. 6358703
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/09/209,916
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-09-209-916-1
Query Match      100.0%; Score 28; DB 2; Length 1438;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
      |||||
Db      814 DYGMS 818

RESULT 26
US-08-670-707A-39
; Sequence 39, Application US/08670707A
; Patent No. 5859204
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,707A
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,133
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 75-95F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-037-601-39
Query Match      100.0%; Score 28; DB 2; Length 1443;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
      |||||
Db      819 DYGMS 823

RESULT 27
US-09-037-601-39
; Sequence 39, Application US/09037601
; Patent No. 6180371
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,601
; FILING DATE: 26-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,133
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 75-95F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-037-601-39
Query Match      100.0%; Score 28; DB 2; Length 1443;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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|
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Db 819 DYGMS 823

RESULT 28

US-09-315-179-39
; Sequence 39, Application US/09315179
; Patent No. 6376463
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95H
; CURRENT APPLICATION NUMBER: US/09/315,179
; EARLIER FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. 09/037,601
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: U.S. 08/670,707
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: PCT/US97/11155
; EARLIER FILING DATE: 1997-06-26
; EARLIER APPLICATION NUMBER: PCT/US94/13200
; EARLIER FILING DATE: 1994-11-15
; EARLIER APPLICATION NUMBER: U.S. 08/212,133
; EARLIER FILING DATE: 1994-03-11
; EARLIER APPLICATION NUMBER: U.S. 07/864,004
; EARLIER FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-315-179-39

Query Match 100.0%; Score 28; DB 2; Length 1443;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
Db 819 DYGMS 823

RESULT 29

US-09-407-605-3
; Sequence 3, Application US/09407605
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; EARLIER FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated peptide
US-09-407-605-3

Query Match 100.0%; Score 28; DB 2; Length 1445;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
Db 821 DYGMS 825

RESULT 30

US-09-407-605-4
; Sequence 4, Application US/09407605
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated peptide
US-09-407-605-4

Query Match 100.0%; Score 28; DB 2; Length 1447;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
Db 823 DYGMS 827

RESULT 31

US-09-001-039B-47
; Sequence 47, Application US/09001039B
; Patent No. 6818439
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Respass, James G.
; APPLICANT: Defolo, Nicholas J.
; APPLICANT: Hsu, David Chi-Tang
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Greengard, Judith
; APPLICANT: Lee, Will
; TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
; TITLE OF INVENTION: RECOMBINANT GENE DELIVERY VEHICLES FOR TREATMENT
; TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/001.039B
/ FILING DATE: 13-JAN-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcmasters, David D.
/ REGISTRATION NUMBER: 33,963
/ REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1457 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-001-039B-47

Query Match 100.0%; Score 28; DB 2; Length 1457;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 833 DYGMS 837

RESULT 32
US-09-523-656-38
/ Sequence 38, Application US/09523656
/ Patent No. 6458563
/ GENERAL INFORMATION:
/ APPLICANT: Lollar S., John
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: 75-951
/ CURRENT APPLICATION NUMBER: US/09/523,656
/ CURRENT FILING DATE: 2000-03-10
/ EARLIER APPLICATION NUMBER: 09/037,601
/ EARLIER FILING DATE: 1998-03-10
/ EARLIER APPLICATION NUMBER: 08/670,707
/ EARLIER FILING DATE: 1996-06-26
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 38
/ LENGTH: 1467
/ TYPE: PRT
/ ORGANISM: Porcine
/ US-09-523-656-38

Query Match 100.0%; Score 28; DB 2; Length 1467;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 843 DYGMS 847

RESULT 33
US-08-683-839B-3
/ Sequence 3, Application US/08683839B
/ Patent No. 5744326
/ GENERAL INFORMATION:
/ APPLICANT: Ill, Charles R. et al
/ TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional
/ TITLE OF INVENTION: Regulatory Sequences To Increase Expression of
/ TITLE OF INVENTION: Introns Genes Containing Near-Consensus Splice Sites
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street, suite 510
/ CITY: Boston

```

```

/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/683,839B
/ FILING DATE: 11-MARCH-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Remillard, Jane E.
/ REGISTRATION NUMBER: 38,872
/ REFERENCE/DOCKET NUMBER: TTI-138
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1471 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-683-839B-3

Query Match 100.0%; Score 28; DB 1; Length 1471;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 847 DYGMS 851

RESULT 34
US-08-882-083-2
/ Sequence 2, Application US/08882083
/ Patent No. 5869292
/ GENERAL INFORMATION:
/ APPLICANT: VOORBERG, Johannes J.
/ TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/882,083
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/558,107
/ FILING DATE: 13-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ISACSON, John P.
/ REGISTRATION NUMBER: 33,715
/ REFERENCE/DOCKET NUMBER: 30472/212
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399

```

TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-882-083-2

Query Match 100.0%; Score 28; DB 1; Length 1661;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 1037 DYGMS 1041

RESULT 35
US-08-558-107-2
Sequence 2, Application US/08558107
Patent No. 5910481
GENERAL INFORMATION:
APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,107
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30472/212
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-558-107-2

Query Match 100.0%; Score 28; DB 1; Length 1661;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 1037 DYGMS 1041

RESULT 36
US-09-243-539-2
Sequence 2, Application US/09243539
Patent No. 6130203
GENERAL INFORMATION:
APPLICANT: VOORBERG, Johannes J.

TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,539
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30472/212
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-243-539-2

Query Match 100.0%; Score 28; DB 2; Length 1661;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 1037 DYGMS 1041

RESULT 37
US-09-324-867-5
Sequence 5, Application US/09324867A
Patent No. 6251632
GENERAL INFORMATION:
APPLICANT: Lillcrap, David
APPLICANT: Cameron, Cherie
APPLICANT: NO. 6251632ley, Colleen
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 2115
TYPE: PRT
ORGANISM: Sus spp.
US-09-324-867-5
Query Match 100.0%; Score 28; DB 2; Length 2115;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 1492 DYGMS 1496

RESULT 38

US-08-670-707A-37
; Sequence 37, Application US/08670707A
; Patent No. 5859204
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670.707A
; FILING DATE: 26-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,133
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 75-95F
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-707A-37

Query Match 100.0%; Score 28; DB 1; Length 2133;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 1509 DYGMS 1513

RESULT 39

US-09-037-601-37
; Sequence 37, Application US/09037601
; Patent No. 6180371
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,601
; FILING DATE: 26-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US94/13200
; FILING DATE: 15-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,133
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 75-95F
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-037-601-37

Query Match 100.0%; Score 28; DB 2; Length 2133;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 1509 DYGMS 1513

RESULT 40

US-09-315-179-37
; Sequence 37, Application US/09315179
; Patent No. 6376463
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95H
; CURRENT APPLICATION NUMBER: US/09/315,179
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. 09/037,601
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: U.S. 08/670,707
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: PCT/US97/11155
; EARLIER FILING DATE: 1997-06-26
; EARLIER APPLICATION NUMBER: PCT/US94/13200
; EARLIER FILING DATE: 1994-11-15
; EARLIER APPLICATION NUMBER: U.S. 08/212,133
; EARLIER FILING DATE: 1994-03-11
; EARLIER APPLICATION NUMBER: U.S. 07/864,004
; EARLIER FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 37
; LENGTH: 2133
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-315-179-37

Query Match      100.0%; Score 28; DB 2; Length 2133;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
      |||||
Db      1509 DYGMS 1513
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Search completed: November 18, 2005, 21:16:56
Job time : 18.8929 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:14:46 ; Search time 53.75 Seconds
(without alignments)
38.868 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

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6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	5	3	US-09-832-312-73
2	28	100.0	5	3	US-09-829-495-73
3	28	100.0	5	4	US-10-032-037B-114
4	28	100.0	5	4	US-10-029-988B-114
5	28	100.0	5	4	US-10-032-423A-114
6	28	100.0	5	4	US-10-029-926B-114
7	28	100.0	5	4	US-10-610-843B-6
8	28	100.0	5	5	US-10-850-034-73
9	28	100.0	20	4	US-10-327-598-445
10	28	100.0	20	4	US-10-433-273-58
11	28	100.0	60	4	US-10-433-273-4
12	28	100.0	98	4	US-10-194-975-20
13	28	100.0	98	4	US-10-308-817-60
14	28	100.0	98	4	US-10-032-037B-61
15	28	100.0	98	4	US-10-029-988B-61
16	28	100.0	98	4	US-10-032-423A-61
17	28	100.0	98	4	US-10-453-698-60
18	28	100.0	98	4	US-10-029-926B-61
19	28	100.0	98	4	US-10-379-392-21
20	28	100.0	98	5	US-10-884-830-599
21	28	100.0	116	4	US-10-437-963-114282
22	28	100.0	123	6	US-11-039-767-12
23	28	100.0	146	5	US-10-909-851-29
24	28	100.0	156	4	US-10-424-599-215325
25	28	100.0	239	3	US-09-880-748-937
26	28	100.0	239	3	US-09-880-748-2015
27	28	100.0	239	3	US-09-880-748-2038
					Sequence 2038, Ap

28	28	100.0	239	4	US-10-293-418-937
29	28	100.0	239	4	US-10-293-418-2015
30	28	100.0	239	4	US-10-293-418-2038
31	28	100.0	242	5	US-10-935-290-130
32	28	100.0	242	6	US-11-017-030-28
33	28	100.0	244	4	US-10-322-673-42
34	28	100.0	244	5	US-10-981-465-42
35	28	100.0	244	5	US-10-981-621-42
36	28	100.0	244	5	US-10-981-673-42
37	28	100.0	244	5	US-10-981-691-42
38	28	100.0	249	5	US-10-935-290-40
39	28	100.0	251	3	US-09-880-748-1542
40	28	100.0	251	4	US-10-293-418-1542
41	28	100.0	266	4	US-10-032-037B-204
42	28	100.0	266	4	US-10-029-988B-204
43	28	100.0	266	4	US-10-032-423A-204
44	28	100.0	276	4	US-10-425-114-70003
45	28	100.0	277	4	US-10-032-037B-25
46	28	100.0	277	4	US-10-032-037B-203
47	28	100.0	277	4	US-10-029-988B-25
48	28	100.0	277	4	US-10-029-988B-203
49	28	100.0	277	4	US-10-032-423A-25
50	28	100.0	277	4	US-10-032-423A-203
51	28	100.0	277	4	US-10-029-926B-25
52	28	100.0	277	4	US-10-029-926B-203
53	28	100.0	279	4	US-10-610-843B-1
54	28	100.0	279	4	US-10-425-114-36951
55	28	100.0	299	4	US-10-767-701-44522
56	28	100.0	300	4	US-10-425-114-37904
57	28	100.0	309	4	US-10-052-798-9
58	28	100.0	309	4	US-10-288-917-9
59	28	100.0	309	4	US-10-423-448-9
60	28	100.0	373	3	US-09-828-995B-35
61	28	100.0	373	4	US-10-753-159-35
62	28	100.0	464	4	US-10-032-037B-26
63	28	100.0	464	4	US-10-029-988B-26
64	28	100.0	464	4	US-10-032-423A-26
65	28	100.0	464	4	US-10-029-926B-26
66	28	100.0	467	4	US-10-425-115-226209
67	28	100.0	470	3	US-09-828-995B-11
68	28	100.0	470	4	US-10-753-159-11
69	28	100.0	474	4	US-10-328-459-4
70	28	100.0	601	4	US-10-282-122A-52207
71	28	100.0	603	5	US-10-732-923-23079
72	28	100.0	605	4	US-10-369-493-19434
73	28	100.0	609	4	US-10-282-122A-76594
74	28	100.0	652	4	US-10-369-493-12803
75	28	100.0	1424	5	US-10-472-916-5
76	28	100.0	1424	5	US-10-968-286-5
77	28	100.0	1431	4	US-10-095-718-4
78	28	100.0	1431	4	US-10-681-970-4
79	28	100.0	1438	4	US-10-006-091-1
80	28	100.0	1438	4	US-10-047-257-1
81	28	100.0	1438	4	US-10-225-900-1
82	28	100.0	1443	4	US-10-187-319-39
83	28	100.0	1443	4	US-10-131-510A-39
84	28	100.0	1443	5	US-10-938-414-39
85	28	100.0	1457	5	US-10-813-507-13
86	28	100.0	1457	5	US-10-813-507-17
87	28	100.0	1459	4	US-10-239-498A-4
88	28	100.0	1459	4	US-10-239-498A-13
89	28	100.0	1459	4	US-10-239-498A-15
90	28	100.0	1467	5	US-10-813-907-4
91	28	100.0	1467	5	US-10-813-907-15
92	28	100.0	1467	5	US-10-813-507-19
93	28	100.0	1467	5	US-10-813-507-21
94	28	100.0	1471	4	US-10-095-718-2
95	28	100.0	1471	4	US-10-681-970-2
96	28	100.0	2096	5	US-10-741-600-1032
97	28	100.0	2114	4	US-10-721-997A-33
98	28	100.0	2114	5	US-10-973-941-3
99	28	100.0	2133	4	US-10-187-319-37
100	28	100.0	2133	4	US-10-131-510A-37

ALIGNMENTS

RESULT 1
US-09-832-312-73
; Sequence 73, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 1999-12-06
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-73

Query Match 100.0%; Score 28; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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|
|
|
|
Db 1 DYGMS 5

RESULT 2
US-09-829-495-73
; Sequence 73, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-02-14
; PRIOR FILING DATE: 1999-12-06
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-73

Query Match 100.0%; Score 28; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
|
Db 1 DYGMS 5

RESULT 3
US-10-032-037B-114
; Sequence 114, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-114

Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
|
Db 1 DYGMS 5

RESULT 4
US-10-029-988B-114
; Sequence 114, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-114

Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|
|
|
|
|
Db 1 DYGMS 5

RESULT 5
US-10-032-423A-114
; Sequence 114, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.

;; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
;; FILE REFERENCE: 10793/45
;; CURRENT APPLICATION NUMBER: US/10/032,423A
;; CURRENT FILING DATE: 2001-12-31
;; PRIOR APPLICATION NUMBER: 60/258,948
;; PRIOR FILING DATE: 12/29/2000
;; NUMBER OF SEQ ID NOS: 204
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 114
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-032-423A-114

Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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DB 1 DYGMS 5

RESULT 6
US-10-029-926B-114
;; Sequence 114, Application US/10029926B
;; Publication No. US20040073011A1
;; GENERAL INFORMATION:
;; APPLICANT: HAGAY, et al.
;; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
;; FILE REFERENCE: 10793/50
;; CURRENT APPLICATION NUMBER: US/10/029,926B
;; CURRENT FILING DATE: 2001-12-31
;; PRIOR APPLICATION NUMBER: 60/258,948
;; PRIOR FILING DATE: 12/29/2000
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 114
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-029-926B-114

Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 1 DYGMS 5

RESULT 7
US-10-610-843B-6
;; Sequence 6, Application US/10610843B
;; Publication No. US20040202665A1
;; GENERAL INFORMATION:
;; APPLICANT: Lazarovits, et al.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
;; FILE REFERENCE: 10793/72
;; CURRENT APPLICATION NUMBER: US/10/610,843B
;; CURRENT FILING DATE: 2003-06-30
;; PRIOR APPLICATION NUMBER: 60/393,453
;; PRIOR FILING DATE: 2002-07-01
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-610-843B-6

Query Match 100.0%; Score 28; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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DB 1 DYGMS 5

RESULT 8
US-10-850-034-73
;; Sequence 73, Application US/108500034
;; Publication No. US20040253236A1
;; GENERAL INFORMATION:
;; APPLICANT: Busfield SJ
;; APPLICANT: Villevall J
;; APPLICANT: Jandrot-Perrus M
;; APPLICANT: Vainchenker W
;; APPLICANT: Gill DS
;; APPLICANT: Qian MD
;; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
;; FILE REFERENCE: 7853-234
;; CURRENT APPLICATION NUMBER: US/10/850,034
;; CURRENT FILING DATE: 2004-05-20
;; PRIOR APPLICATION NUMBER: US/09/829,495
;; PRIOR FILING DATE: 2001-04-09
;; PRIOR APPLICATION NUMBER: 09/610,118
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: 09/503,387
;; PRIOR FILING DATE: 2000-02-14
;; PRIOR APPLICATION NUMBER: 09/454,824
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 09/345,468
;; PRIOR FILING DATE: 1999-06-30
;; NUMBER OF SEQ ID NOS: 78
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 73
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-850-034-73

Query Match 100.0%; Score 28; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 1 DYGMS 5

RESULT 9
US-10-327-598-445
;; Sequence 445, Application US/10327598
;; Publication No. US20040181039A1
;; GENERAL INFORMATION:
;; APPLICANT: Krah, Eugene
;; APPLICANT: Guo, Honliang
;; APPLICANT: Aiyappa, Ashok
;; APPLICANT: Lawton, Robert
;; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
;; TITLE OF INVENTION: for Making and Using Them
;; FILE REFERENCE: 01-799-A
;; CURRENT APPLICATION NUMBER: US/10/327,598
;; CURRENT FILING DATE: 2002-12-20
;; PRIOR APPLICATION NUMBER: US 60/344,874
;; PRIOR FILING DATE: 2001-12-21
;; NUMBER OF SEQ ID NOS: 1139
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 445
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: canis familiaris;

US-10-327-598-445

Query Match 100.0%; Score 28; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 18; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
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Db 6 DYGMs 10

RESULT 10

US-10-433-273-58
; Sequence 58, Application US/10433273

; Publication No. US20040096456A1

; GENERAL INFORMATION:

; APPLICANT: Regents of the University of Minnesota

; APPLICANT: Conti-Fine, Bianca M.

; TITLE OF INVENTION: Methods to Treat Hemophilia

; FILE REFERENCE: 600.507W01

; CURRENT APPLICATION NUMBER: US/10/433,273

; CURRENT FILING DATE: 2003-11-17

; PRIOR APPLICATION NUMBER: US 60/250,430

; PRIOR FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 61

; SEQ ID NO 58

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-433-273-58

Query Match 100.0%; Score 28; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 37; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
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Db 9 DYGMs 13

RESULT 11

US-10-433-273-4

; Sequence 4, Application US/10433273

; Publication No. US20040096456A1

; GENERAL INFORMATION:

; APPLICANT: Regents of the University of Minnesota

; APPLICANT: Conti-Fine, Bianca M.

; TITLE OF INVENTION: Methods to Treat Hemophilia

; FILE REFERENCE: 600.507W01

; CURRENT APPLICATION NUMBER: US/10/433,273

; CURRENT FILING DATE: 2003-11-17

; PRIOR APPLICATION NUMBER: US 60/250,430

; PRIOR FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 61

; SEQ ID NO 4

; LENGTH: 60

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-433-273-4

Query Match 100.0%; Score 28; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
| | | | |
Db 39 DYGMs 43

RESULT 12

US-10-194-975-20

; Sequence 20, Application US/10194975

; Publication No. US20030039649A1

; GENERAL INFORMATION:

; APPLICANT: Foote, Jefferson

; TITLE OF INVENTION: Super Humanized Antibodies

; FILE REFERENCE: 501231.01

; CURRENT APPLICATION NUMBER: US/10/194,975

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: US 60/305,111

; PRIOR FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-194-975-20

Query Match 100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
| | | | |
Db 31 DYGMs 35

RESULT 13

US-10-308-817-60

; Sequence 60, Application US/10308817

; Publication No. US20030219861A1

; GENERAL INFORMATION:

; APPLICANT: Rother, Russell

; APPLICANT: Wu, Dayang

; TITLE OF INVENTION: HYBRID ANTIBODIES

; FILE REFERENCE: 1087-37

; CURRENT APPLICATION NUMBER: US/10/308,817

; CURRENT FILING DATE: 2002-12-03

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 60

; LENGTH: 98

; TYPE: PRT

; ORGANISM: human

US-10-308-817-60

Query Match 100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
| | | | |
Db 31 DYGMs 35

RESULT 14

US-10-032-037B-61

; Sequence 61, Application US/10032037B

; Publication No. US20040001822A1

; GENERAL INFORMATION:

; APPLICANT: Bio-Technology General Corp.

; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

; FILE REFERENCE: 10793/44

; CURRENT APPLICATION NUMBER: US/10/032,037B

; CURRENT FILING DATE: 2001-12-31

; PRIOR APPLICATION NUMBER: 60/258,948

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 61

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-032-037B-61

```
Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY      1 DYGMS 5
      |||||
Db      31 DYGMS 35

RESULT 15
US-10-029-988B-61
; Sequence 61, Application US/10029988B
; Publication No. US2004001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-61

Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY      1 DYGMS 5
      |||||
Db      31 DYGMS 35

RESULT 16
US-10-032-423A-61
; Sequence 61, Application US/10032423A
; Publication No. US2004002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-61

Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY      1 DYGMS 5
      |||||
Db      31 DYGMS 35

RESULT 17
US-10-453-698-60
; Sequence 60, Application US/10453698
```

```
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-453-698-60

Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY      1 DYGMS 5
      |||||
Db      31 DYGMS 35

RESULT 18
US-10-029-926B-61
; Sequence 61, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-61

Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY      1 DYGMS 5
      |||||
Db      31 DYGMS 35

RESULT 19
US-10-379-392-21
; Sequence 21, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahivat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
```

```
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-21

Query Match      100.0%; Score 28; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
DB      31 DYGMS 35

RESULT 20
US-10-884-830-599
; Sequence 599, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Saifeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-599

Query Match      100.0%; Score 28; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
DB      31 DYGMS 35

RESULT 21
US-10-437-963-114282
; Sequence 114282, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114282
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17989C.1.pep
US-10-437-963-114282

Query Match      100.0%; Score 28; DB 4; Length 116;
```

```
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
DB      62 DYGMS 66

RESULT 22
US-11-039-767-12
; Sequence 12, Application US/11039767
; Publication No. US20050170398A1
; GENERAL INFORMATION:
; APPLICANT: CRUCCELL HOLLAND B.V.
; TITLE OF INVENTION: Recombinant production of mixtures of antibodies
; FILE REFERENCE: 0079 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/039,767
; CURRENT FILING DATE: 2005-01-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH sequence of clone B28 (anti-CD22 phage)
US-11-039-767-12

Query Match      100.0%; Score 28; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
DB      33 DYGMS 37

RESULT 23
US-10-909-851-29
; Sequence 29, Application US/10909851
; Publication No. US20050170334A1
; GENERAL INFORMATION:
; APPLICANT: Kirin Brewery Co.
; APPLICANT: Mikayama, Toshifumi
; APPLICANT: Wang, Rongfang
; APPLICANT: Kato, Shinichiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INFLUENZA M2 PROTEIN AND METHODS C
; TITLE OF INVENTION: AND USING SAME
; FILE REFERENCE: 021286-0309187
; CURRENT APPLICATION NUMBER: US/10/909,851
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: 60/364,997
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 10/389,221
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: PCT/US03/08147
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-851-29

Query Match      100.0%; Score 28; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
DB      50 DYGMS 54
```

RESULT 24
US-10-424-599-215325
; Sequence 215325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215325
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(156)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36463C.1.pep
US-10-424-599-215325

Query Match 100.0%; Score 28; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 121 DYGMS 125

RESULT 25
US-09-880-748-937
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match 100.0%; Score 28; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 31 DYGMS 35

RESULT 26
US-09-880-748-2015
; Sequence 2015, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2015
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2015

Query Match 100.0%; Score 28; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 31 DYGMS 35

RESULT 27
US-09-880-748-2038
; Sequence 2038, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2038

Query Match 100.0%; Score 28; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 31 DYGMS 35

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2015

Query Match      100.0%; Score 28; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
        |||||
Db      31 DYGMS 35

RESULT 28
US-10-293-418-937
; Sequence 937, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match      100.0%; Score 28; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
        |||||
Db      31 DYGMS 35

RESULT 29
US-10-293-418-2015
; Sequence 2015, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2015
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2015

Query Match      100.0%; Score 28; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
        |||||
Db      31 DYGMS 35

RESULT 30
US-10-293-418-2038
; Sequence 2038, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2038

Query Match      100.0%; Score 28; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYGMS 5
        |||||
Db      31 DYGMS 35

RESULT 31
US-10-935-290-130
; Sequence 130, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PF584P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 130
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-935-290-130

```


; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMCC127
US-10-935-290-130

Query Match 100.0%; Score 28; DB 5; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 31 DYGMS 35

RESULT 32

US-11-017-030-28
; Sequence 28, Application US/11017030
; Publication No. US20050158313A1
; GENERAL INFORMATION:

; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Reg IV

; FILE REFERENCE: PF592PCT
; CURRENT APPLICATION NUMBER: US/11/017,030
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: PCT/US03/19908
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 60/392,382
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 242

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: scFv protein RGC0115

US-11-017-030-28

Query Match 100.0%; Score 28; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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DB 31 DYGMS 35

RESULT 33

US-10-322-673-42
; Sequence 42, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 42
; LENGTH: 244

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-322-673-42

Query Match 100.0%; Score 28; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||
DB 31 DYGMS 35

RESULT 34

US-10-981-465-42
; Sequence 42, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

; FILE REFERENCE: PF585P1
; CURRENT APPLICATION NUMBER: US/10/981,465
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-465-42

Query Match 100.0%; Score 28; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
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DB 31 DYGMS 35

RESULT 35

US-10-981-621-42
; Sequence 42, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:

; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

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; FILE REFERENCE: PF585PID1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-621-42

Query Match          100.0%; Score 28; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 36
US-10-981-673-42
; Sequence 42, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-621-42

Query Match          100.0%; Score 28; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 36
US-10-981-673-42
; Sequence 42, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-691-42

Query Match          100.0%; Score 28; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 37
US-10-981-691-42
; Sequence 42, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID3
; CURRENT APPLICATION NUMBER: US/10/981,691
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-691-42

Query Match          100.0%; Score 28; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYGMS 5
Db      31 DYGMS 35

RESULT 38
US-10-935-290-40
; Sequence 40, Application US/10935290
; Publication No. US20050069542A1
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; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PF584PI
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 40
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMBC603
US-10-935-290-40

Query Match 100.0%; Score 28; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
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Db 31 DYGM5 35

RESULT 39
US-09-880-748-1542
; Sequence 1542, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1542
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1542

Query Match 100.0%; Score 28; DB 3; Length 251;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
|||
Db 31 DYGM5 35

RESULT 40
US-10-293-418-1542
; Sequence 1542, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1542
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1542

Query Match 100.0%; Score 28; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
|||
Db 31 DYGM5 35

Search completed: November 18, 2005, 21:40:04
Job time : 55.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:15:38 ; Search time 1.42857 Seconds
(without alignments)
3.954 Million cell updates/sec

Title: US-10-029-926D-114
Perfect score: 28
Sequence: 1 DYGMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:

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2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pap:
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pap:
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8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	474	US-11-008-331-4	Sequence 4, Appl
2	24	85.7	123	US-10-131-826A-402	Sequence 402, App
3	24	85.7	770	US-10-982-545-15	Sequence 15, Appl
4	24	85.7	770	US-10-789-273-38	Sequence 38, Appl
5	23	82.1	138	US-10-789-273-4	Sequence 4, Appl
6	23	82.1	138	US-10-789-273-8	Sequence 8, Appl
7	23	82.1	138	US-10-789-273-12	Sequence 12, Appl
8	22	78.6	240	US-10-689-742-210	Sequence 210, App
9	22	78.6	396	US-11-109-156-10	Sequence 10, Appl
10	22	78.6	464	US-10-689-742-164	Sequence 164, App
11	22	78.6	473	US-11-074-176-338	Sequence 338, App
12	22	78.6	487	US-11-074-176-130	Sequence 130, App
13	22	78.6	545	US-11-065-943-63	Sequence 63, Appl
14	22	78.6	545	US-11-065-943-65	Sequence 65, Appl
15	22	78.6	545	US-11-065-943-67	Sequence 67, Appl
16	22	78.6	545	US-11-065-943-69	Sequence 69, Appl
17	22	78.6	545	US-11-065-943-71	Sequence 71, Appl
18	22	78.6	545	US-11-065-943-73	Sequence 73, Appl
19	22	78.6	545	US-11-065-943-75	Sequence 75, Appl
20	22	78.6	545	US-11-065-943-77	Sequence 77, Appl
21	22	78.6	545	US-11-065-943-79	Sequence 79, Appl
22	22	78.6	545	US-11-065-943-81	Sequence 81, Appl
23	22	78.6	545	US-11-065-943-83	Sequence 83, Appl
24	22	78.6	545	US-11-065-943-85	Sequence 85, Appl
25	22	78.6	545	US-11-065-943-87	Sequence 87, Appl

26	78.6	545	7	US-11-065-943-89	Sequence 89, Appl
27	78.6	545	7	US-11-065-943-91	Sequence 91, Appl
28	78.6	545	7	US-11-065-943-93	Sequence 93, Appl
29	78.6	545	7	US-11-065-943-95	Sequence 95, Appl
30	78.6	545	7	US-11-065-943-97	Sequence 97, Appl
31	78.6	545	7	US-11-065-943-99	Sequence 99, Appl
32	78.6	562	7	US-11-065-943-20	Sequence 20, Appl
33	78.6	562	7	US-11-065-943-22	Sequence 22, Appl
34	78.6	562	7	US-11-065-943-24	Sequence 24, Appl
35	78.6	562	7	US-11-065-943-26	Sequence 26, Appl
36	78.6	562	7	US-11-065-943-28	Sequence 28, Appl
37	78.6	562	7	US-11-065-943-30	Sequence 30, Appl
38	78.6	562	7	US-11-065-943-32	Sequence 32, Appl
39	78.6	562	7	US-11-065-943-34	Sequence 34, Appl
40	78.6	562	7	US-11-065-943-36	Sequence 36, Appl
41	78.6	562	7	US-11-065-943-38	Sequence 38, Appl
42	78.6	625	7	US-10-131-826A-70	Sequence 70, Appl
43	78.6	832	7	US-11-065-943-100	Sequence 100, App
44	75.0	174	7	US-11-074-176-264	Sequence 264, App
45	75.0	199	1	US-10-510-386-248	Sequence 248, App
46	75.0	221	7	US-11-102-978-11	Sequence 11, Appl
47	75.0	456	7	US-11-021-441-18	Sequence 18, Appl
48	75.0	479	7	US-11-021-441-20	Sequence 20, Appl
49	75.0	490	7	US-11-021-441-22	Sequence 22, Appl
50	75.0	497	7	US-11-021-441-24	Sequence 24, Appl
51	75.0	503	7	US-11-082-389-290	Sequence 290, App
52	75.0	503	7	US-11-082-389-362	Sequence 362, App
53	75.0	697	7	US-11-082-389-362	Sequence 362, App
54	75.0	987	1	US-10-949-720-395	Sequence 395, App
55	75.0	1035	7	US-11-021-441-4	Sequence 4, Appl
56	75.0	2314	7	US-11-013-759-11	Sequence 11, Appl
57	71.4	116	7	US-11-174-186-2	Sequence 2, Appl
58	71.4	116	7	US-11-174-186-4	Sequence 4, Appl
59	71.4	116	7	US-11-174-186-6	Sequence 6, Appl
60	71.4	116	7	US-11-174-186-17	Sequence 17, Appl
61	71.4	116	7	US-11-174-186-18	Sequence 18, Appl
62	71.4	116	7	US-11-174-186-19	Sequence 19, Appl
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64	71.4	116	7	US-11-174-186-22	Sequence 22, Appl
65	71.4	116	7	US-11-174-186-23	Sequence 23, Appl
66	71.4	116	7	US-11-174-186-24	Sequence 24, Appl
67	71.4	116	7	US-11-174-186-25	Sequence 25, Appl
68	71.4	116	7	US-11-174-186-26	Sequence 26, Appl
69	71.4	116	7	US-11-174-186-35	Sequence 35, Appl
70	71.4	117	1	US-10-648-816-9	Sequence 9, Appl
71	71.4	118	1	US-10-648-816-14	Sequence 14, Appl
72	71.4	121	1	US-10-648-816-15	Sequence 15, Appl
73	71.4	121	1	US-10-648-816-15	Sequence 15, Appl
74	71.4	154	7	US-11-082-389-424	Sequence 424, App
75	71.4	216	7	US-11-082-389-32	Sequence 32, Appl
76	71.4	244	1	US-10-510-386-110	Sequence 110, App
77	71.4	318	7	US-11-109-156-15	Sequence 15, Appl
78	71.4	421	1	US-10-131-826A-302	Sequence 302, App
79	71.4	477	1	US-10-131-826A-452	Sequence 452, App
80	71.4	511	7	US-11-012-762-66	Sequence 66, Appl
81	71.4	511	7	US-11-152-747-4	Sequence 4, Appl
82	71.4	543	7	US-10-495-664-3	Sequence 3, Appl
83	71.4	579	7	US-11-174-186-41	Sequence 41, Appl
84	71.4	718	7	US-11-074-176-306	Sequence 306, App
85	71.4	723	7	US-11-074-176-18	Sequence 18, Appl
86	71.4	1344	7	US-11-091-643-20	Sequence 20, Appl
87	71.4	1386	7	US-11-091-643-6	Sequence 6, Appl
88	67.9	12	7	US-11-016-706-46	Sequence 46, Appl
89	67.9	21	1	US-10-939-890-542	Sequence 542, App
90	67.9	21	1	US-10-939-890-771	Sequence 771, App
91	67.9	25	1	US-10-939-890-489	Sequence 489, App
92	67.9	25	1	US-10-939-890-649	Sequence 649, App
93	67.9	25	1	US-10-939-890-859	Sequence 859, App
94	67.9	55	1	US-10-997-201A-14	Sequence 14, Appl
95	67.9	98	7	US-11-144-248-30	Sequence 30, Appl
96	67.9	118	1	US-10-648-816-10	Sequence 10, Appl
97	67.9	118	1	US-10-648-816-12	Sequence 12, Appl
98	67.9	118	1	US-10-648-816-13	Sequence 13, Appl

99 19 67.9 121 1 US-10-648-816-16 Sequence 16, Appl
100 19 67.9 121 7 US-11-077-978-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-11-008-331-4
; Sequence 4, Application US/11008331
; Publication No. US20050244925A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC386-PCT
; CURRENT APPLICATION NUMBER: US/11/008,331
; PRIOR FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: EP9719637.2
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Schizocaccharomyces pombe
US-11-008-331-4

Query Match 100.0%; Score 28; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0

Qy 1 DYGMS 5
Db 349 DYGMS 353

RESULT 2

US-10-131-826A-402
; Sequence 402, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 402
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-402

Query Match 85.7%; Score 24; DB 1; Length 123;
Best Local Similarity 80.0%; Pred. No. 6.6; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0

Qy 1 DYGMS 5
Db 51 DYGMS 55

RESULT 3

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE

LOCATION: (1)...(40)
OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)...(687)
OTHER INFORMATION: soluble APP-alpha
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)...(671)
OTHER INFORMATION: soluble APP-beta
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)...(770)
OTHER INFORMATION: C99
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)...(711)
OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)...(770)
OTHER INFORMATION: C83
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)...(713)
OTHER INFORMATION: P3(42)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)...(711)
OTHER INFORMATION: P3(40)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (712)...(770)
OTHER INFORMATION: gamma-CTF(59)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)...(770)
OTHER INFORMATION: gamma-CTF(57)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (721)...(770)
OTHER INFORMATION: gamma-CTF(50)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)...(770)
OTHER INFORMATION: C31
US-10-982-545-15

Query Match 85.7%; Score 24; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 4
Db 167 DYGM 170

RESULT 4
US-10-789-273-38
Sequence 38, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 85.7%; Score 24; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 4
Db 167 DYGM 170

RESULT 5
US-10-789-273-4
Sequence 4, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 138
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-789-273-4

Query Match 82.1%; Score 23; DB 1; Length 138;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM 5
Db 50 NYGMS 54

RESULT 6
US-10-789-273-8
Sequence 8, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted

;; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
;; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
;; FILE REFERENCE: ELN-002CP
;; CURRENT APPLICATION NUMBER: US/10/789,273
;; CURRENT FILING DATE: 2004-02-27
;; PRIOR APPLICATION NUMBER: US/10/388,389
;; PRIOR FILING DATE: 2003-03-12
;; PRIOR APPLICATION NUMBER: US 10/010,942
;; PRIOR FILING DATE: 2001-12-06
;; PRIOR APPLICATION NUMBER: US 60/251,892
;; PRIOR FILING DATE: 2000-12-06
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-8

Query Match 82.1%; Score 23; DB 1; Length 138;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMs 5
Db 50 NYGMs 54

RESULT 7
US-10-789-273-12
;; Sequence 12, Application US/10789273
;; Publication No. US20050249725A1
;; GENERAL INFORMATION:
;; APPLICANT: Basi, Gurig
;; APPLICANT: Saidanha, Jose
;; APPLICANT: Yednock, Ted
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
;; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
;; FILE REFERENCE: ELN-002CP
;; CURRENT APPLICATION NUMBER: US/10/789,273
;; CURRENT FILING DATE: 2004-02-27
;; PRIOR APPLICATION NUMBER: US/10/388,389
;; PRIOR FILING DATE: 2003-03-12
;; PRIOR APPLICATION NUMBER: US 10/010,942
;; PRIOR FILING DATE: 2001-12-06
;; PRIOR APPLICATION NUMBER: US 60/251,892
;; PRIOR FILING DATE: 2000-12-06
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Humanized 3D6 light chain variable region
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-12

Query Match 82.1%; Score 23; DB 1; Length 138;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMs 5
Db 50 NYGMs 54

RESULT 8
US-10-689-742-210
;; Sequence 210, Application US/10689742
;; Publication No. US20050250180A1
;; GENERAL INFORMATION:
;; APPLICANT: Jacobs, Kenneth
;; APPLICANT: McCoy, John M
;; APPLICANT: Lavallie, Edward R
;; APPLICANT: Racie, Lisa A
;; APPLICANT: Evans, Cheryl
;; APPLICANT: Merberg, David
;; APPLICANT: Treacy, Maurice
;; APPLICANT: Spaulding, Vikki
;; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;; FILE REFERENCE: 00766.000091.10
;; CURRENT APPLICATION NUMBER: US/10/689,742
;; CURRENT FILING DATE: 2003-10-22
;; PRIOR APPLICATION NUMBER: 03/746,783
;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 231
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 210
;; LENGTH: 240
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-689-742-210

Query Match 78.6%; Score 22; DB 1; Length 240;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DYGMs 5
Db 145 DYGSs 149

RESULT 9
US-11-109-156-10
;; Sequence 10, Application US/11109156
;; Publication No. US20050250144A1
;; GENERAL INFORMATION:
;; APPLICANT: Toshio Ota
;; APPLICANT: Takao Isogai
;; APPLICANT: Tetsuo Nishikawa
;; APPLICANT: Koji Hayashi
;; APPLICANT: Kaoru Otsuka
;; APPLICANT: Jun-ichi Yamamoto
;; APPLICANT: Shizuko Ishii
;; APPLICANT: Tomoyasu Sugiyama
;; APPLICANT: Ai Wakamatsu
;; APPLICANT: Keiichi Nagai
;; APPLICANT: Tetsuji Otsuki
;; APPLICANT: Shin-ichi Funahashi
;; APPLICANT: Chitaki Senoo
;; APPLICANT: Jun-ichi Nezu
;; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
;; TITLE OF INVENTION: PHOSPHATASE
;; FILE REFERENCE: 06501-099002
;; CURRENT APPLICATION NUMBER: US/11/109,156
;; CURRENT FILING DATE: 2005-04-19
;; PRIOR APPLICATION NUMBER: US/10/060,065
;; PRIOR FILING DATE: 2002-01-29
;; PRIOR APPLICATION NUMBER: PCT/JP00/05061
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 60/159,590
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: US 60/183,322
;; PRIOR FILING DATE: 2000-02-17
;; PRIOR APPLICATION NUMBER: JP 11-248036
;; PRIOR FILING DATE: 1999-07-29
;; PRIOR APPLICATION NUMBER: JP 2000-118776
;; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-10

Query Match 78.6%; Score 22; DB 7; Length 396;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
Db 197 DYGLA 201

RESULT 10
US-10-689-742-164
; Sequence 164, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Werberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-164

Query Match 78.6%; Score 22; DB 1; Length 464;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
Db 141 YGMS 144

RESULT 11
US-11-074-176-338
; Sequence 338, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161

; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-338

Query Match 78.6%; Score 22; DB 7; Length 473;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYGM5 5
Db 371 DYNMS 375

RESULT 12
US-11-074-176-130
; Sequence 130, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-130

Query Match 78.6%; Score 22; DB 7; Length 487;
Best Local Similarity 80.0%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYGM5 5
Db 385 DYNMS 389

RESULT 13
US-11-065-943-63
; Sequence 63, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426US0XCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 545
; TYPE: PRT

; ORGANISM: Thermus aquaticus
US-11-065-943-63

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|||
Db 382 YGMS 385

RESULT 14

US-11-065-943-65
; Sequence 65, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-65

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|||
Db 382 YGMS 385

RESULT 15

US-11-065-943-67
; Sequence 67, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-67

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|||
Db 382 YGMS 385

RESULT 16

US-11-065-943-69
; Sequence 69, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-69

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|||
Db 382 YGMS 385

RESULT 17

US-11-065-943-71
; Sequence 71, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-71

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|||
Db 382 YGMS 385

RESULT 18

US-11-065-943-73

; Sequence 73, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-73

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGMS 5
Db 382 YGMS 385

RESULT 19
US-11-065-943-75
; Sequence 75, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-75

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGMS 5
Db 382 YGMS 385

RESULT 20
US-11-065-943-77
; Sequence 77, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-77

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGMS 5
Db 382 YGMS 385

RESULT 21
US-11-065-943-79
; Sequence 79, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-79

Query Match 78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGMS 5
Db 382 YGMS 385

RESULT 22
US-11-065-943-81
; Sequence 81, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27

; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 81
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Thermus aquaticus
 US-11-065-943-81

Query Match 78.6%; Score 22; DB 7; Length 545;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
 ||||
 Db 382 YGMS 385

RESULT 23
 ; Sequence 83, Application US/11065943
 ; Publication No. US20050250131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JESTIN, JEAN-LUC
 ; APPLICANT: VICHIER-GUERRE, SOPHIE
 ; APPLICANT: FERRIS, STEPHANE
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
 ; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
 ; FILE REFERENCE: 266426USOXCIP
 ; CURRENT APPLICATION NUMBER: US/11/065,943
 ; CURRENT FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: US 10/787,219
 ; PRIOR FILING DATE: 2004-02-27
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 83
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Thermus aquaticus
 US-11-065-943-83

Query Match 78.6%; Score 22; DB 7; Length 545;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
 ||||
 Db 382 YGMS 385

RESULT 24
 ; Sequence 85, Application US/11065943
 ; Publication No. US20050250131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JESTIN, JEAN-LUC
 ; APPLICANT: VICHIER-GUERRE, SOPHIE
 ; APPLICANT: FERRIS, STEPHANE
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
 ; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
 ; FILE REFERENCE: 266426USOXCIP
 ; CURRENT APPLICATION NUMBER: US/11/065,943
 ; CURRENT FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: US 10/787,219
 ; PRIOR FILING DATE: 2004-02-27
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 85
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Thermus aquaticus
 US-11-065-943-85

Query Match 78.6%; Score 22; DB 7; Length 545;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
 ||||
 Db 382 YGMS 385

RESULT 25
 ; Sequence 87, Application US/11065943
 ; Publication No. US20050250131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JESTIN, JEAN-LUC
 ; APPLICANT: VICHIER-GUERRE, SOPHIE
 ; APPLICANT: FERRIS, STEPHANE
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
 ; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
 ; FILE REFERENCE: 266426USOXCIP
 ; CURRENT APPLICATION NUMBER: US/11/065,943
 ; CURRENT FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: US 10/787,219
 ; PRIOR FILING DATE: 2004-02-27
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 87
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Thermus aquaticus
 US-11-065-943-87

Query Match 78.6%; Score 22; DB 7; Length 545;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
 ||||
 Db 382 YGMS 385

RESULT 26
 ; Sequence 89, Application US/11065943
 ; Publication No. US20050250131A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JESTIN, JEAN-LUC
 ; APPLICANT: VICHIER-GUERRE, SOPHIE
 ; APPLICANT: FERRIS, STEPHANE
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
 ; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
 ; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
 ; FILE REFERENCE: 266426USOXCIP
 ; CURRENT APPLICATION NUMBER: US/11/065,943
 ; CURRENT FILING DATE: 2005-02-25
 ; PRIOR APPLICATION NUMBER: US 10/787,219
 ; PRIOR FILING DATE: 2004-02-27
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 89
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Thermus aquaticus
 US-11-065-943-89

Query Match 78.6%; Score 22; DB 7; Length 545;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
 ||||

Db 382 YGMS 385

RESULT 27

US-11-065-943-91
; Sequence 91, Application US/11065943
; Publication No. US20050250131A1

GENERAL INFORMATION:

; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus

US-11-065-943-91

Query Match

Best Local Similarity 78.6%; Score 22; DB 7; Length 545;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5

Db 382 YGMS 385

RESULT 28

US-11-065-943-93
; Sequence 93, Application US/11065943
; Publication No. US20050250131A1

GENERAL INFORMATION:

; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus

US-11-065-943-93

Query Match

Best Local Similarity 78.6%; Score 22; DB 7; Length 545;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5

Db 382 YGMS 385

RESULT 29

US-11-065-943-95
; Sequence 95, Application US/11065943
; Publication No. US20050250131A1

; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus

US-11-065-943-95

Query Match

Best Local Similarity 78.6%; Score 22; DB 7; Length 545;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5

Db 382 YGMS 385

RESULT 30

US-11-065-943-97
; Sequence 97, Application US/11065943
; Publication No. US20050250131A1

GENERAL INFORMATION:

; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus

US-11-065-943-97

Query Match

Best Local Similarity 78.6%; Score 22; DB 7; Length 545;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5

Db 382 YGMS 385

RESULT 31

US-11-065-943-99
; Sequence 99, Application US/11065943
; Publication No. US20050250131A1

GENERAL INFORMATION:

; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

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/ FILE REFERENCE: 266426USOXCIPI
/ CURRENT APPLICATION NUMBER: US/11/065,943
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: US 10/787,219
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 99
/ LENGTH: 545
/ TYPE: PRT
/ ORGANISM: Thermus aquaticus
US-11-065-943-99

Query Match          78.6%; Score 22; DB 7; Length 545;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 YGMS 5
Db   382 YGMS 385

RESULT 32
US-11-065-943-20
/ Sequence 20, Application US/11065943
/ Publication No. US20050250131A1
/ GENERAL INFORMATION:
/ APPLICANT: JESTIN, JEAN-LUC
/ APPLICANT: VICHIER-GUERRE, SOPHIE
/ TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
/ TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
/ TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
/ FILE REFERENCE: 266426USOXCIPI
/ CURRENT APPLICATION NUMBER: US/11/065,943
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: US 10/787,219
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 20
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Thermus aquaticus
US-11-065-943-20

Query Match          78.6%; Score 22; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 YGMS 5
Db   394 YGMS 397

RESULT 33
US-11-065-943-22
/ Sequence 22, Application US/11065943
/ Publication No. US20050250131A1
/ GENERAL INFORMATION:
/ APPLICANT: JESTIN, JEAN-LUC
/ APPLICANT: VICHIER-GUERRE, SOPHIE
/ TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
/ TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
/ TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
/ FILE REFERENCE: 266426USOXCIPI
/ CURRENT APPLICATION NUMBER: US/11/065,943
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: US 10/787,219
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: PatentIn version 3.3
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/ SEQ ID NO 22
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Thermus aquaticus
US-11-065-943-22

Query Match          78.6%; Score 22; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 YGMS 5
Db   394 YGMS 397

RESULT 34
US-11-065-943-24
/ Sequence 24, Application US/11065943
/ Publication No. US20050250131A1
/ GENERAL INFORMATION:
/ APPLICANT: JESTIN, JEAN-LUC
/ APPLICANT: VICHIER-GUERRE, SOPHIE
/ TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
/ TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
/ TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
/ FILE REFERENCE: 266426USOXCIPI
/ CURRENT APPLICATION NUMBER: US/11/065,943
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: US 10/787,219
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 24
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Thermus aquaticus
US-11-065-943-24

Query Match          78.6%; Score 22; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 YGMS 5
Db   394 YGMS 397

RESULT 35
US-11-065-943-26
/ Sequence 26, Application US/11065943
/ Publication No. US20050250131A1
/ GENERAL INFORMATION:
/ APPLICANT: JESTIN, JEAN-LUC
/ APPLICANT: VICHIER-GUERRE, SOPHIE
/ TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
/ TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
/ TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
/ FILE REFERENCE: 266426USOXCIPI
/ CURRENT APPLICATION NUMBER: US/11/065,943
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: US 10/787,219
/ PRIOR FILING DATE: 2004-02-27
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 26
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Thermus aquaticus
US-11-065-943-26

Query Match          78.6%; Score 22; DB 7; Length 562;
```


; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-36

Query Match 78.6%; Score 22; DB 7; Length 562;
Best Local Similarity 100.0%; Pred.No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGMS 5
|
|
|
|
Db 394 YGMS 397

Search completed: November 18, 2005, 21:40:17
Job time : 2.42857 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:58:55, Search time 10.3571 Seconds
(without alignments)
46.449 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: PIR 80:
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	98	2 S26928	Ig heavy chain V r
2	28	100.0	112	2 PH1654	Ig heavy chain V r
3	28	100.0	119	2 A43413	Ig heavy chain V r
4	28	100.0	227	2 AB1076	probable fibrial
5	28	100.0	268	2 H84684	En/Spm-like transp
6	28	100.0	268	2 T04660	hypothetical prote
7	28	100.0	334	2 H95307	arginine deiminase
8	28	100.0	340	2 H72681	hypothetical prote
9	28	100.0	411	2 S74760	hypothetical prote
10	28	100.0	448	2 AB3043	oxidoreductase Atu
11	28	100.0	468	2 B98243	hypothetical prote
12	28	100.0	474	2 T38737	probable CAXA pren
13	28	100.0	478	2 F89651	protein T04F8.2 (l
14	28	100.0	502	2 T24471	hypothetical prote
15	28	100.0	609	2 H71285	probable cell divi
16	28	100.0	650	2 G87572	calcium-binding pr
17	28	100.0	756	2 D96527	protein F2J7J15.24
18	28	100.0	830	2 I50455	prolactin receptor
19	28	100.0	869	2 A25945	coagulation factor
20	28	100.0	916	2 B84473	copia-like retroel
21	28	100.0	1008	2 H85055	probable transposo
22	28	100.0	1250	2 T27706	hypothetical prote
23	28	100.0	2133	2 T42763	coagulation factor
24	28	100.0	2319	2 A47004	coagulation factor
25	28	100.0	2351	1 EZHU	coagulation factor
26	25	89.3	109	2 T47696	hypothetical prote
27	25	89.3	113	2 B36259	Ig heavy chain V r
28	25	89.3	136	2 S35759	BHD9D10 protein -
29	25	89.3	138	1 D69979	conserved hypothet

30	25	89.3	145	2 D69383	conserved hypothet
31	25	89.3	154	2 B61027	hypothetical prote
32	25	89.3	171	2 S69895	helicase (EC 3.6.1
33	25	89.3	188	2 T48671	extracellular heme
34	25	89.3	203	2 T05519	hypothetical prote
35	25	89.3	203	2 C85288	hypothetical prote
36	25	89.3	220	2 H81048	biopolymer transp
37	25	89.3	233	1 F69178	conserved hypothet
38	25	89.3	238	2 H70734	hypothetical prote
39	25	89.3	250	2 C85040	RNA polymerase sig
40	25	89.3	251	2 D69861	phosphoglycolate p
41	25	89.3	264	2 AF3550	hypothetical prote
42	25	89.3	277	2 S76396	hypothetical prote
43	25	89.3	289	2 AI3166	hypothetical prote
44	25	89.3	291	2 A69545	mRNA 3'-end proces
45	25	89.3	298	2 T29685	hypothetical prote
46	25	89.3	303	2 T20425	hypothetical prote
47	25	89.3	321	2 T44336	hypothetical prote
48	25	89.3	323	2 S61927	lipase A precursor
49	25	89.3	328	2 S70885	UDP-galactose 4-ep
50	25	89.3	332	2 F95937	probable murein pep
51	25	89.3	334	2 D83164	conserved hypothet
52	25	89.3	344	2 C82835	anthranilate phosph
53	25	89.3	347	2 G95146	conserved domain p
54	25	89.3	347	2 E98014	conserved hypothet
55	25	89.3	352	2 C37471	hypothetical helic
56	25	89.3	357	2 A80104	lactose operon rep
57	25	89.3	368	2 D87271	general secretion
58	25	89.3	371	2 B97094	NAD-dependent 4-hy
59	25	89.3	379	2 A49679	exo-alpha-sialidas
60	25	89.3	392	2 T30026	hypothetical prote
61	25	89.3	394	2 AB0713	probable membrane
62	25	89.3	412	2 B97077	diverged AAA-famil
63	25	89.3	417	2 I84434	Rhesus-like protei
64	25	89.3	426	2 AS0907	cytosine deaminase
65	25	89.3	429	2 T34466	hypothetical prote
66	25	89.3	442	2 T34661	hypothetical prote
67	25	89.3	458	2 E82340	probable gluconate
68	25	89.3	472	2 S53866	cytosine methylase
69	25	89.3	477	2 J80029	nitrogenase molybd
70	25	89.3	484	2 AG3184	aldehyde dehydroge
71	25	89.3	490	2 E71486	probable s/t prote
72	25	89.3	496	1 A46725	omega-crystallin -
73	25	89.3	499	2 F72768	probable gamma-glu
74	25	89.3	506	2 AC3255	1-sorbose dehydr
75	25	89.3	512	2 S19354	cell fusion protei
76	25	89.3	520	2 T20007	hypothetical prote
77	25	89.3	544	2 T23968	hypothetical prote
78	25	89.3	558	2 S29125	alkaline phosphata
79	25	89.3	564	2 F87305	gamma-glutamyltran
80	25	89.3	581	2 E91165	gamma-glutamyltran
81	25	89.3	581	2 E86011	hypothetical prote
82	25	89.3	581	2 T23396	hypothetical prote
83	25	89.3	619	2 D69194	PER112-like protei
84	25	89.3	632	2 T48316	hypothetical prote
85	25	89.3	632	2 T31667	guanylate cyclase
86	25	89.3	632	2 T31666	natriuretic peptid
87	25	89.3	645	2 E96631	probable receptor
88	25	89.3	657	2 G86799	hypothetical prote
89	25	89.3	691	2 AD2766	conserved hypothet
90	25	89.3	691	2 H97546	hypothetical 81.9K
91	25	89.3	698	2 AB3576	fusaric acid resis
92	25	89.3	719	2 T47727	hypothetical prote
93	25	89.3	719	2 B86490	F28222.6 protein -
94	25	89.3	836	2 T46070	hypothetical prote
95	25	89.3	836	2 AB1270	DNA polymerase I l
96	25	89.3	875	2 AG1632	DNA polymerase I l
97	25	89.3	876	2 G89952	DNA polymerase I l
98	25	89.3	876	2 A84044	DNA polymerase I p
99	25	89.3	880	2 E69680	DNA polymerase I p
100	25	89.3	880	2 T42600	DNA helicase/prima

ALIGNMENTS

RESULT 1

Ig heavy chain V region (DP-32) - human (fragment)
A/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26928
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26928
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <IOM>
A/Cross-references: UNIPARC:UPI0000116409; EMBL:Z12334; NID:G32887; PIDN:CAA78204.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 31 DYGMS 35

RESULT 2

Ig heavy chain V region (clone 6H9) - human (fragment)
A/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1654
R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1654
A/Molecule type: mRNA
A/Residues: 1-112 <HIL>
A/Cross-references: UNIPARC:UPI0000176BDB
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 23 DYGMS 27

RESULT 3

Ig heavy chain V region - mouse (fragment)
A/Species: Mus musculus (house mouse)
C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C/Accession: A43413
R/Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kun
J. Biol. Chem. 267, 18085-18092, 1992
A/Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A/Reference number: A43413; MUID:92388177; PMID:1517241
A/Accession: A43413
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-119 <TOM>

A/Cross-references: UNIPARC:UPI0000176C37
A/Note: sequence extracted from NCBI backbone (NCBIP:112815)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:9-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 28; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 25 DYGMS 29

RESULT 4

AB1076
probable fimbrial chaperone protein sthB [imported] - Salmonella enterica subsp. enteric
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB1076
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pichard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.W.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB1076
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-227 <PAR>
A/Cross-references: UNIPARC:UPI000005A9F4; G8:AL513382; PIDN:CAD03425.1; PID:g16505691;
C/Genetics:
A/Gene: sthB
C/Superfamily: chaperone protein papD

Query Match 100.0%; Score 28; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
| | | | |
Db 215 DYGMS 219

RESULT 5

H84684
En/Spm-like transposon protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: H84684
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84684
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-268 <SPO>
A/Cross-references: UNIPROT:Q9SKM6; UNIPARC:UPI00000AA595; GB:AE002093; NID:g4432833; P
C/Genetics:
A/Map position: 2

Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5

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Db          218 DYGMS 222
|||||
RESULT 6
T04660
hypothetical protein F8D20.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04660
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15381
A:Accession: T04660
A:Molecule type: DNA
A:Residues: 1-268 <BEV>
A:CROSS-references: UNIPROT:O81788; UNIPARC:UPI00000AC5E8; EMBL:AL031135
A:Experimental source: cultivar Columbia; BAC clone F8D20
C:Genetics:
A:Map position: 4
A:Introns: 75/1; 241/1
A:Note: F8D20.60

Query Match          100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 263 DYGMS 267
|||||

RESULT 7
H95307
arginine deiminase (EC 3.5.3.6) ArcB [imported] - Sinorhizobium meliloti (strain 1021) m
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004
C:Accession: H95307
R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bove
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95307
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:CROSS-references: UNIPROT:Q92ZT1; UNIPARC:UPI00000CB093; GB:AE006469; PIDN:AAK65026.1;
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: arcB
A:Genome: plasmid
C:Superfamily: ornithine/aspartate carbamoyltransferase; aspartate/ornithine carbamoyltr
C:Keywords: hydrolase

Query Match          100.0%; Score 28; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 292 DYGMS 296
|||||

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RESULT 8
H72681
hypothetical protein APE0874 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H72681
R:Kawarayayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72681
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <KAW>
A:CROSS-references: UNIPROT:Q9YDP1; UNIPARC:UPI000005DD0D; DBJ:AP000060; NID:G5104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0874
C:Superfamily: Aeropyrum pernix hypothetical protein APE0874

Query Match          100.0%; Score 28; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 82 DYGMS 86
|||||

RESULT 9
S74760
hypothetical protein elr1617 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74760
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasu
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74760
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KAN>
A:CROSS-references: UNIPROT:P72895; UNIPARC:UPI00000C0C3B; EMBL:D90901; GB:AB001339; NI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match          100.0%; Score 28; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
Db 65 DYGMS 69
|||||

RESULT 10
AB3043
oxidoreductase Atu3958 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AB3043
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193

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A;Accession: AB3043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <KUR>
A;Cross-references: UNIPROT:Q8U8Y0; UNIPARC:UPI000001648AE; GB:AE008689; PIDN:AAL44760.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3958
A;Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 124 DYGMS 128

RESULT 11
B98243
hypothetical protein AGR_L1791 [imported] - Agrobacterium tumefaciens (strain C58, 'Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98243
A;Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B98243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <KUR>
A;Cross-references: UNIPROT:Q8U8Y0; UNIPARC:UPI00000023BC; GB:AE007870; PIDN:AAK89468.1;
C;Genetics:
A;Gene: AGR_L1791
A;Map position: linear chromosome

Query Match 100.0%; Score 28; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 144 DYGMS 148

RESULT 12
T38737
Probable CAAX prenyl proteinase 1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38737
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z21808
A;Accession: T38737
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-474 <GEN>
A;Cross-references: UNIPROT:Q10071; UNIPARC:UPI0000003174B; EMBL:Z68144; PIDN:CAA92258.1;
A;Experimental source: strain 972h-; cosmid C3H1
C;Genetics:
A;Gene: SPDB:SPAC3H1.05
A;Map position: 1
A;Introns: 35/3

Query Match 100.0%; Score 28; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5

Db 349 DYGMS 353

RESULT 13
F89651
protein T04F8.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89651
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F89651
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-478 <STO>
A;Cross-references: UNIPROT:Q22162; UNIPARC:UPI0000179353; GB:chr_X; PIDN:CAA91478.1; PI
A;Note: cDNA EST EMBL:MB9094 comes from this gene
C;Genetics:
A;Gene: T04F8.2
A;Map position: X
C;Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 77 DYGMS 81

RESULT 14
T24471
hypothetical protein T04F8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24471
R;Lennard, N.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19895
A;Accession: T24471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-502 <WIL>
A;Cross-references: UNIPROT:Q22162; UNIPARC:UPI0000074D3A; EMBL:Z66565; PIDN:CAA91478.2;
A;Experimental source: clone T04F8
C;Genetics:
A;Gene: C89P:T04F8.2
A;Map position: X
A;Introns: 26/1; 72/1; 103/3; 162/2; 214/3; 249/2; 290/2; 340/3; 382/2; 427/1; 459/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T04F8.2

Query Match 100.0%; Score 28; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.le+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 93 DYGMS 97

RESULT 15
H71285
probable cell division protein (ftsH) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: H71285
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rsen, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDevitt, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71285
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-609 <COM>
A:CROSS-references: UNIPROT:O83746; UNIPARC:UPI000012ACDC; GB:AE000520; NID:F153-363/Domain: FtSH/SEC18/CDC48-type ATP-binding domain homology <VAR>
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0765
C:Superfamily: cell division protein ftsH; FtsH/SEC18/CDC48-type ATP-binding domain homology
F:153-363/Domain: FtSH/SEC18/CDC48-type ATP-binding domain homology <VAR>

Query Match 100.0%; Score 28; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
DB 493 DYGMS 497

RESULT 16
G87572
calcium-binding protein [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: G87572
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonitskii, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-650 <STO>
A:CROSS-references: UNIPROT:Q9A554; UNIPARC:UPI00000C77A6; GB:AE005673; NID:g13424183; F:153-363/Domain: FtSH/SEC18/CDC48-type ATP-binding domain homology <VAR>
C:Genetics:
A:Gene: CC2610

Query Match 100.0%; Score 28; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
DB 272 DYGMS 276

RESULT 17
D96527
protein F77J15.24 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D96527
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96527
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-756 <STO>
A:CROSS-references: UNIPROT:Q9W999; UNIPARC:UPI00000A6A1A; GB:AE005173; NID:g7770335; F:153-363/Domain: FtSH/SEC18/CDC48-type ATP-binding domain homology <VAR>
C:Genetics:
A:Gene: F27J15.24
A:Map position: 1

Query Match 100.0%; Score 28; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
DB 728 DYGMS 732

RESULT 18
I50455
prolactin receptor - pigeon
C:Species: *Columba livia* (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CH>
A:CROSS-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:g466381; F:153-363/Domain: FtSH/SEC18/CDC48-type ATP-binding domain homology <VAR>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 100.0%; Score 28; DB 2; Length 830;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
DB 77 DYGMS 81

RESULT 19
A25945
coagulation factor VIII - pig (fragment)
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 31-Dec-2004
C:Accession: A25945
R:Toole, J.J.; Pittman, D.D.; Orr, E.C.; Murtha, P.; Wasley, L.C.; Kaufman, R.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 5939-5942, 1986
A:Title: A large region (approx 195 kDa) of human factor VIII is dispensable for in vitro coagulation.
A:Reference number: A25945; MUID:86287369; PMID:3016730
A:Accession: A25945
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-869 <TOO>
A:CROSS-references: UNIPROT:P12263; UNIPARC:UPI00001752D8
C:Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxi

Query Match 100.0%; Score 28; DB 2; Length 869;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||||
DB 805 DYGMS 809

RESULT 20
B84473
copla-like retroelement pol polyprotein [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84473
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, J.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84473
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-916 <STO>
A;Cross-references: UNIPROT:Q9ZUF5; UNIPARC:UPI00000A2DA5; GB:AE002093; NID:G4006828; PI
C;Genetics:
A;Gene: AT2G05930
A;Map position: 2

Query Match 100.0%; Score 28; DB 2; Length 916;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 830 DYGMS 834

RESULT 21
H85055
Probable transposon protein [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85055
R;Anonymous, The European Union *Arabidopsis* Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1008 <STO>
A;Cross-references: UNIPROT:Q9XEC0; UNIPARC:UPI00000AAA79; GB:NC_001268; NID:G7267199; F
C;Genetics:
A;Gene: AT4G04420
A;Map position: 4

Query Match 100.0%; Score 28; DB 2; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 922 DYGMS 926

RESULT 22
T27706
Hypothetical protein ZK1193.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27706
R;Gaisel, C.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of *C. elegans* cosmid ZK1193.
A;Reference number: 220409
A;Accession: T27706
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1250 <GBI>
A;Cross-references: UNIPROT:Q23409; UNIPARC:UPI00000785EE; EMBL:U41553; PIDN:AAA83291.1;
C;Genetics:
A;Gene: CESF:ZK1193.2
A;Introns: 95/2; 228/1; 302/1; 355/2; 388/1; 400/1; 451/1; 514/1; 593/1; 643/3; 822/2; 8

Query Match 100.0%; Score 28; DB 2; Length 1250;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 893 DYGMS 897

RESULT 23
T42763
coagulation factor VIII precursor - pig
C;Species: *Sus scrofa domestica* (domestic pig)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 31-Dec-2004
C;Accession: T42763
R;Lollar, P.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z22269
A;Accession: T42763
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2133 <LOL>
A;Cross-references: UNIPROT:PI2263; UNIPARC:UPI000012A417; EMBL:U49517; NID:G1511633; PI
C;Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxid
C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2133/Product: coagulation factor VIII #status predicted <MAT>
F;23-349/Domain: ferroxidase repeat homology <FOX1>
F;402-730/Domain: ferroxidase repeat homology <FOX2>
F;1498-1820/Domain: ferroxidase repeat homology <FOX3>

Query Match 100.0%; Score 28; DB 2; Length 2133;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 1509 DYGMS 1513

RESULT 24
A47004
coagulation factor VIII precursor - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 31-Dec-2004
C;Accession: A47004
R;Elder, B.; Laskich, D.; Gitschier, J.
Genomics 16, 374-379, 1993
A;Title: Sequence of the murine factor VIII cDNA.
A;Reference number: A47004; MUID:93300511; PMID:8314577
A;Accession: A47004
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2319 <ELD>
A;Cross-references: UNIPROT:Q06194; UNIPARC:UPI00000275E4; GB:L05573; NID:G192456; PIDN:7
C;Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;23-349/Domain: ferroxidase repeat homology <FO1>
F;402-730/Domain: ferroxidase repeat homology <FO2>
F;1686-2006/Domain: ferroxidase repeat homology <FO3>
F;2007-2156/Domain: discoidin I amino-terminal homology <DN1>
F;2160-2313/Domain: discoidin I amino-terminal homology <DN2>

Query Match 100.0%; Score 28; DB 2; Length 2319;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 1697 DYGMS 1701

RESULT 25

EZHU
coagulation factor VIII precursor [validated] - human
N:Alternate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant compo
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 31-Dec-2004
C:Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; B42
R:Gieschier, J.; Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 1992
A:Title: Sequence of the exon-containing regions of the human factor VIII gene.
A:Reference number: I54318; MUID:93265012; PMID:1303178
A:Accession: I54318
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1921, 'S', 1923-2351 <RES>
A:Cross-references: UNIPROT: P00451; UNIPARC:UPI000016A8D3; GB:M88648; NID:gl82381; PIDN:
R:Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.B.; Gieschier, J.; Keyt, B.; Seeburg
Nature 312, 330-337, 1984
A:Title: Expression of active human factor VIII from recombinant DNA clones.
A:Reference number: A00525; MUID:85061548; PMID:6438526
A:Accession: A00525
A:Molecule type: mRNA
A:Residues: 1-2351 <WOO>
A:Cross-references: UNIPARC:UPI000012A416; EMBL:X01165; EMBL:X01166; EMBL:X01179
R:Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.;
S. D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A:Title: Molecular cloning of a cDNA encoding human antihemophilic factor.
A:Reference number: I58059; MUID:85061550; PMID:6438528
A:Accession: I58059
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RE2>
A:Cross-references: UNIPARC:UPI0000144860; GB:X01740; NID:gl82802; PIDN:AAAS2484.1; PID:
R:Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo,
B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favalaro, J.; Hansen, J.; No
DNA 4, 333-349, 1985
A:Title: Characterization of the polypeptide composition of human factor VIII:C and the
A:Reference number: A23584; MUID:86081164; PMID:3935400
A:Accession: A23584
A:Molecule type: mRNA
A:Residues: 1-2351 <TRU>
A:Cross-references: UNIPARC:UPI000012A416; GB:M14113; NID:gl82817; PIDN:AAAS2485.1; PID:
R:Eaton, D.; Rodriguez, H.; Vehar, G.A.
Biochemistry 25, 505-512, 1986
A:Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages
ity.
A:Reference number: A26174; MUID:86159740; PMID:3082357
A:Accession: A26174
A:Molecule type: protein
A:Residues: 20-36;392-399, 'X', 401-402;1668-1678;1709-1722, 'D', 1723-1725;1741-1755 <EAT>
A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI0000172297; UNIPARC:UPI0000172298;
R:Pittman, D.D.; Wang, J.H.; Kaufman, R.J.
Biochemistry 31, 3315-3325, 1992
A:Title: Identification and functional importance of tyrosine sulfate residues within re
A:Reference number: A42348; MUID:92207952; PMID:1554716
A:Accession: A42348
A:Molecule type: protein
A:Residues: 20-36;356-371;392-408;582-594;1668-1669, 'X', 1671;1672-1692;1693-1708;1709-17
A:Cross-references: UNIPARC:UPI0000172296; UNIPARC:UPI0000172298; UNIPARC:UPI0000172299;
2A1
A:Experimental source: recombinant material from Chinese hamster ovary cells
A:Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
R:Pay, P.J.; Smudzin, T.M.
J. Biol. Chem. 264, 14005-14010, 1989
A:Title: Intersubunit fluorescence energy transfer in human factor VIII.
A:Reference number: A43986; MUID:89340500; PMID:2503509
A:Accession: A43986
A:Molecule type: protein
A:Residues: 'X', 517-523;1853-1860, 'X', 1862-1864, 'X', 1866 <FAY>
A:Cross-references: UNIPARC:UPI00001722A2; UNIPARC:UPI00001722A3
R:Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens, K.;
J. Biol. Chem. 266, 740-746, 1991
A:Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for

A:Reference number: A56109; MUID:91093266; PMID:1898735
A:Contents: annotation; sulfation
R:Gieschier, J.; Wood, W.I.; Goralka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,
Nature 312, 326-330, 1984
A:Title: Characterization of the human factor VIII gene.
A:Reference number: A56196; MUID:85061547; PMID:6438525
A:Contents: annotation; introns
R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
Protein Sci. 4, 740-746, 1995
A:Title: Locations of disulfide bonds and free cysteines in the heavy and light chains o
A:Reference number: A56216; MUID:95338127; PMID:7613471
A:Contents: annotation; disulfide bonds
A:Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
R:Kjalk, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
Eur. J. Biochem. 234, 773-779, 1995
A:Title: Amino acid residues 721-729 are required for full factor VIII activity.
A:Reference number: S63527; MUID:96163459; PMID:8575434
A:Accession: S63527
A:Molecule type: protein
A:Residues: 733-752;753-759 <KJA>
A:Cross-references: UNIPARC:UPI00001722A4; UNIPARC:UPI00001722A5
R:Lind, P.; Larsson, K.; Spira, J.; Sydow-Baekman, M.; Almqvist, A.; Gray, E.; Sandber,
Eur. J. Biochem. 232, 19-27, 1995
A:Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
A:Reference number: S66445; MUID:96048024; PMID:7556150
A:Accession: S66445
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1668-1685 <LIN>
A:Cross-references: UNIPARC:UPI00001722A6
A:Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure p
C:Genetics:
A:Gene: GDB:F8C
A:Cross-references: GDB:119124; OMIM:306700
A:Map position: Xq28-Xq28
A:Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 6
C:Function:
A:Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pr
A:Pathway: blood coagulation
C:Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxi
C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pl
F:1-19/Domain: signal sequence status predicted <SIG>
F:20-2351/Product: coagulation factor VIII #status experimental <WAT>
F:20-740/Product: coagulation factor VIII heavy chain #status experimental <ACH>
F:20-356/Domain: A1 <DA1>
F:23-348/Domain: ferroxidase repeat homology <FO1>
F:392-759/Domain: A2 <DA2>
F:402-730/Domain: ferroxidase repeat homology <FO2>
F:760-1667/Domain: B <DB0>
F:1668-2351/Product: coagulation factor VIIIa light chain #status experimental <ACL>
F:1709-2038/Domain: A3 <DA3>
F:1716-2038/Domain: ferroxidase repeat homology <FO3>
F:2039-2191/Domain: C1 <DC1>
F:2039-2188/Domain: discoidin I amino-terminal homology <DNI>
F:2192-2351/Domain: C2 <DC2>
F:2192-2345/Domain: discoidin I amino-terminal homology <DN2>
F:60-258, 601, 776, 803, 847, 919, 962, 982, 1020, 1024, 1074, 1085, 1204, 1274, 1278, 1301, 1319, 1403,
F:172-198, 267-348, 547-573, 649-730, 1851-1877, 1918-1922, 2040-2188/Disulfide bonds: #statu
F:355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) #status predicted
F:365-737, 738, 742, 1683, 1699/Binding site: sulfate (Tyr) (covalent) #status experimental
F:391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F:414, 426/Binding site: sulfate (Tyr) (covalent) #status predicted
F:759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F:1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) #status experimental
F:1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F:1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) #status experimental
F:2193-2345/Disulfide bonds: #status predicted

Query Match 100.0%; Score 28; DB 1; Length 2351;

Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMS 5

Db 1727 DYGMS 1731
|||||
RESULT 26
T47696
hypothetical protein T22E16.230 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47696
R;Banes, V.; Wurbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24472
A;Accession: T47696
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <BEN>
A;Cross-references: UNIPROT:Q9M2S2; UNIPARC:UPI000000A5517; EMBL:AL132975
A;Experimental source: cultivar Columbia; BAC clone T22E16
C;Genetics:
A;Map position: 3
A;Introns: 17/1
A;Note: T22E16.230
Query Match 89.3%; Score 25; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
|||||
Db 60 DYGLS 64
RESULT 27
B36259
Ig heavy chain V region TE34 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 21-Jan-2000
C;Accession: B36259
R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A;Title: NMR-derived model for a peptide-antibody complex.
A;Reference number: A36259; MUID:91104915; PMID:2271636
A;Accession: B36259
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <ZIL>
A;Cross-references: UNIPARC:UPI0000176916; GB:M30458; GB:M30459; GB:M30480; GB:M30481; G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Query Match 89.3%; Score 25; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
|||||
Db 31 DYGMN 35
RESULT 28
S35759
BHD9D10 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S35759
R;Froyen, G.F.V.
submitted to the EMBL Data Library, May 1993
A;Reference number: S35759
A;Accession: S35759
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-136 <PRO>
A;Cross-references: UNIPARC:UPI0000113799; EMBL:X72796; NID:g312496; PIDN:CAA51316.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
Query Match 89.3%; Score 25; DB 2; Length 136;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
|||||
Db 50 DYGMN 54
RESULT 29
D69979
conserved hypothetical protein yrrK - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: D69979
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Wintere, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69979
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-138 <KUN>
A;Cross-references: UNIPROT:O34634; UNIPARC:UPI0000060816; GB:Z99117; GB:Z99118; GB:AL00
A;Experimental source: strain 168
C;Genetics:
A;Gene: yrrK
C;Superfamily: Haemophilus influenzae conserved hypothetical protein HI0305
Query Match 89.3%; Score 25; DB 1; Length 138;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
|||||
Db 39 DYGLS 43
RESULT 30
D69383
conserved hypothetical protein AFI068 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69383
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69383
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-145 <KLE>

A;Cross-references: UNIPROT:O29194; UNIPARC:UPI0000056B84; GB:AE001029; GB:AE000782; NID: C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0206

Query Match 89.3%; Score 25; DB 2; Length 145;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
|||:|
Db 69 DYGLS 73

RESULT 31
B61027
hypothetical protein 154 - fava bean mitochondrion
C;Species: mitochondrion Vicia faba (fava bean)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: B61027
R;Macfarlane, J.L.; Wahleithner, J.A.; Wolstenholme, D.R.
Curr. Genet. 18, 87-91, 1990
A;Title: A broad bean mitochondrial atp6 gene with an unusually simple, non-conserved 5'
A;Reference number: A61027; MUID:91059426; PMID:2245478
A;Accession: B61027
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <MAC>
A;Cross-references: UNIPROT:Q04655; UNIPARC:UPI000013B96A; GB:X54285; NID:gl4117; PIDN: C
A;Note: the authors translated the codon CGG for residue 72 as Trp
C;Genetics:
A;Genome: mitochondrion
C;Keywords: mitochondrion

Query Match 89.3%; Score 25; DB 2; Length 154;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
|||:|
Db 44 DYGLS 48

RESULT 32
S69895
helicase (EC 3.6.1.-) - cottontail rabbit herpesvirus (isolate CTHV263) (fragment)
C;Species: cottontail rabbit herpesvirus
A;Variety: isolate CTHV263
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 26-Aug-1999
C;Accession: S69895; S69893
R;Foulon, T.; Pertuiset, B.; Cajean-Peroldi, C.; Sheldrick, P.
Virus Res. 29, 115-124, 1993
A;Title: Possible relation between the U(54) segment of the CTHV genome and the conserve
A;Reference number: S69894; MUID:94025938; PMID:8212854
A;Accession: S69895
A;Molecule type: DNA
A;Residues: 1-171 <FOU>
A;Cross-references: UNIPARC:UPI00000F8349; EMBL:M88073; NID:g349445; PIDN:AAA75555.1; PI
A;Experimental source: isolate CTHV263
R;Foulon, T.T.F.
submitted to the EMBL Data Library, September 1990
A;Reference number: S70036
A;Accession: S69893
A;Molecule type: DNA
A;Residues: 1-126 <POW>
A;Cross-references: UNIPARC:UPI00000ED836; EMBL:X55709; NID:g510495; PIDN:CAA39242.1; PI
C;Superfamily: varicella-zoster virus gene 55 protein
C;Keywords: DNA binding; DNA repair; DNA replication; hydrolase

Query Match 89.3%; Score 25; DB 2; Length 171;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGM5 5
|||:|

Db 73 DYGLS 77

RESULT 33

T48671
extracellular heme acquisition protein hasA [validated] - Serratia marcescens
C;Species: Serratia marcescens
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: T48671

R;Letoffe, S.; Ghigo, J.M.; Wandersman, C.

Proc. Natl. Acad. Sci. U.S.A. 91, 9876-9880, 1994

A;Title: Iron acquisition from heme and hemoglobin by a Serratia marcescens extracellular

A;Reference number: Z24524; MUID:95024064; PMID:7937909

A;Accession: T48671

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-188 <LET>

A;Cross-references: UNIPROT:Q54450; UNIPARC:UPI0000110739; EMBL:X81195; PIDN:CAA57068.1

A;Experimental source: strain SM365

C;Genetics:

A;Gene: hasA

C;Function:

A;Description: required for heme acquisition [validated, MUID:95024064]

C;Superfamily: Serratia marcescens heme acquisition protein hasA

C;Keywords: extracellular protein; heme binding

A;Accession: C85288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <STO>
A;Cross-references: UNIPROT:Q9SW28; UNIPARC:UPI00000A587E; GB:NC_001268; NID:g7269348; F
C;Genetics:
A;Gene: AT4g24980
A;Map position: 4

Query Match 89.3%; Score 25; DB 2; Length 203;

Best Local Similarity 80.0%; Pred. No. 2.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 1 DYGMS 5
|||:|
DB 38 DYGLS 42

RESULT 36

H81048 biopolymer transport protein ExbB NMB1729 [imported] - Neisseria meningitidis (strain MC

C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: H81048; E81827

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:2017555; PMID:10710307

A;Accession: H81048

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-220 <TET>

A;Cross-references: UNIPROT:P57027; UNIPARC:UPI000012A340; GB:AE002523; GB:AE002098; NID

A;Experimental source: serogroup B, strain MC58

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:2022556; PMID:10761919

A;Accession: E81827

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-220 <PAR>

A;Cross-references: UNIPARC:UPI000012A340; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:

A;Experimental source: serogroup A, strain Z2491

C;Genetics:

A;Gene: exbB; NMB1729; NMA1984

C;Superfamily: biopolymer transport protein

Query Match 89.3%; Score 25; DB 2; Length 220;

Best Local Similarity 80.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 1 DYGMS 5
|||:|
DB 121 DYGMT 125

RESULT 37

F69178 conserved hypothetical protein MTH593 - Methanobacterium thermoautotrophicum (strain Del

C;Species: Methanobacterium thermoautotrophicum

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: F69178

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

. A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: F69178

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <MTH>

A;Cross-references: UNIPROT:Q26693; UNIPARC:UPI0000066621; GB:AE000841; GB:AE000666; NID

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH593

C;Superfamily: conserved hypothetical protein MTH593

Query Match 89.3%; Score 25; DB 1; Length 233;

Best Local Similarity 80.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 1 DYGMS 5
|||:|
DB 61 DYGLS 65

RESULT 38

H70734

hypothetical protein Rv2308 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: H70734

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70734

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-238 <COL>

A;Cross-references: UNIPROT:Q50657; UNIPARC:UPI000013BA5E; GB:Z77163; GB:AL123456; NID:g

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv2308

Query Match 89.3%; Score 25; DB 2; Length 238;

Best Local Similarity 80.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 1 DYGMS 5
|||:|
DB 212 DYGLS 216

RESULT 39

C85040

hypothetical protein AT4g03170 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: C85040

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: C85040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250 <STO>

A;Cross-references: UNIPROT:Q9ZR14; UNIPARC:UPI000009F46A; GB:NC_001268; NID:g7270187; P

C;Genetics:

A;Gene: AT4g03170

A;Map position: 4

Query Match 89.3%; Score 25; DB 2; Length 250;

Best Local Similarity 80.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

QY 1 DYGMS 5
|||:
Db 214 DYGLS 218

RESULT 40

D69861
RNA polymerase sigma factor homolog ykoZ - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69861
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
R:Kunst, F.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69861
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-251 <KUN>
A:Cross-references: UNIPROT:O31654; UNIPARC:UPI00000602D0; GB:Z99111; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: ykoZ

Query Match 89.3%; Score 25; DB 2; Length 251;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
|||:
Db 159 DYGLS 163

Search completed: November 18, 2005, 21:15:24
Job time : 14.3571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:58:05 ; Search time 64.8214 Seconds
(without alignments)
54.421 Million cell updates/sec

Title: US-10-029-926D-114

Perfect score: 28

Sequence: 1 DYGMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	70	Q84247_ORYSA	Q84247 oryza sativ
2	28	100.0	112	Q9HCC1_HUMAN	Q9hcc1 homo sapien
3	28	100.0	122	Q4W515_CAEEL	Q4w515 caenorhabdi
4	28	100.0	195	Q726K5_DESVH	Q726k5 desulfovibr
5	28	100.0	204	Q08823_MOUSE	Q08823 mus musculu
6	28	100.0	204	Q08826_MOUSE	Q08826 mus musculu
7	28	100.0	206	Q69X89_ORYSA	Q69x89 oryza sativ
8	28	100.0	227	Q57G17_SALCH	Q57g17 salmonella
9	28	100.0	227	Q5PNA2_SALPA	Q5pna2 salmonella
10	28	100.0	227	Q8Z0S8_SALTI	Q8z0s8 salmonella
11	28	100.0	227	Q8ZJU0_SALTY	Q8zju0 salmonella
12	28	100.0	242	Q6GR19_XENLA	Q6gr19 xenopus lae
13	28	100.0	245	Q6E260_ARATH	Q6e260 arabidopsis
14	28	100.0	246	Q6NU71_XENLA	Q6nu71 xenopus lae
15	28	100.0	249	Q8E110_STRAS	Q8e110 streptococc
16	28	100.0	255	Q6GM50_XENLA	Q6gm50 xenopus lae
17	28	100.0	263	Q4KT14_9NUCL	Q4kt14 chrysodeixi
18	28	100.0	268	Q0X133_ARATH	Q0x133 arabidopsis
19	28	100.0	268	Q9SKM6_ARATH	Q9skm6 arabidopsis
20	28	100.0	280	Q742X5_MYCPA	Q742x5 mycobacteri
21	28	100.0	293	Q8PFN0_XANAC	Q8pfno xanthomonas
22	28	100.0	300	Q9C840_ARATH	Q9c840 arabidopsis
23	28	100.0	302	Q9M7X8_ARATH	Q9m7x8 arabidopsis
24	28	100.0	323	Q54KM8_DICDI	Q54km8 dictyosteli
25	28	100.0	333	Q4JAU3_SULAC	Q4jau3 sulfolobus
26	28	100.0	333	Q6LI62_PICTO	Q6li62 pictophilus
27	28	100.0	334	Q1TCC_RHIME	Q1tcc rhizobium m
28	28	100.0	340	Q9YDF1_AERPE	Q9ydf1 aeropyrum p
29	28	100.0	342	Q4NRK8_9DELT	Q4nrk8 anaeromyxob
30	28	100.0	350	Q4HT34_CAMUP	Q4ht34 campylobact
31	28	100.0	352	Q4IEG8_GIBZE	Q4ieg8 gibberella

32	28	100.0	352	Q5MD63_BOVIN	Q5md63 bos taurus
33	28	100.0	352	Q6YT41_PIG	Q6yt41 sus scrofa
34	28	100.0	354	CCRS_MOUSE	P51682 mus musculu
35	28	100.0	354	Q5RI50_MOUSE	Q5ris0 mus musculu
36	28	100.0	361	Q7CCF5_ECOLE	Q7ccf5 escherichia
37	28	100.0	362	Q9LTC3_ARATH	Q9lct3 arabidopsis
38	28	100.0	406	Q9EYS9_9RHIZ	Q9eys9 rhizobium s
39	28	100.0	411	Q72895_SYNY3	P72895 synecocyst
40	28	100.0	411	Q87T65_VIBPA	Q87t65 vibrio para
41	28	100.0	439	Q4WU03_ASPFU	Q4wu03 aspergillus
42	28	100.0	440	Q4QBX6_LEISHA	Q4qbx6 leishmania
43	28	100.0	448	Q8UB80_AGRIS	Q8ub80 agrobacteri
44	28	100.0	448	Q880T6_PSESM	Q880t6 pseudomonas
45	28	100.0	468	Q7CTQ2_AGRIS	Q7ctq2 agrobacteri
46	28	100.0	474	STE24_SCHPO	Q10071 schizosacch
47	28	100.0	486	Q8L4E4_ORYSA	Q8l4e4 oryza sativ
48	28	100.0	493	QCLN_XENLA	Q9pun1 xenopus lae
49	28	100.0	502	Q610V8_CABER	Q610v8 caenorhabdi
50	28	100.0	502	Q22162_CABEL	Q22162 caenorhabdi
51	28	100.0	512	Q526M9_MAGGR	Q526m9 magnaporthe
52	28	100.0	516	Q4IFE6_GIBZE	Q4ife6 gibberella
53	28	100.0	517	Q6CCU2_YARLI	Q6ccu2 yarrowia li
54	28	100.0	519	Q66J48_XENLA	Q66j48 xenopus lae
55	28	100.0	520	Q5B922_EMENI	Q5b922 aspergillus
56	28	100.0	532	Q7XR43_ORYSA	Q7xr43 oryza sativ
57	28	100.0	537	Q4Y4B8_PLACH	Q4y4b8 plasmodium
58	28	100.0	537	Q91F86_IRV6	Q91f86 chilo iride
59	28	100.0	539	Q55T34_CRYNE	Q55t34 cryptococcu
60	28	100.0	539	Q5KHG4_CRYNE	Q5khg7 cryptococcu
61	28	100.0	560	Q6FEU4_ACIAD	Q6feu4 acinetobact
62	28	100.0	572	P87247_BOTCI	Q944b7 botrytis ci
63	28	100.0	572	Q98AA9_RHILO	Q98aa9 rhizobium l
64	28	100.0	603	Q899H3_CLOTE	Q899h3 clostridium
65	28	100.0	609	FTSH_TREPA	Q83746 treponema p
66	28	100.0	628	Q5NHT6_FRATH	Q5nht8 francisella
67	28	100.0	650	Q9A554_CAUCR	Q9a554 caulobacter
68	28	100.0	658	Q73QH3_TREDE	Q73qhn3 treponema d
69	28	100.0	728	Q7URM7_USTMA	Q7urm7 rhodopirell
70	28	100.0	742	Q4P6A2_USTMA	Q4p6a2 ustilago ma
71	28	100.0	756	Q9M999_ARATH	Q9m999 arabidopsis
72	28	100.0	813	Q6CK12_KJULA	Q6ck12 kluyveromyc
73	28	100.0	830	PLRL_COLLI	Q90374 columba liv
74	28	100.0	885	PLSB_XANAC	Q8pse0 xanthomonas
75	28	100.0	886	Q5H6B2_XANOR	Q5h6b2 xanthomonas
76	28	100.0	916	Q9ZUF5_ARATH	Q9zuf5 arabidopsis
77	28	100.0	1008	Q9XEC0_ARATH	Q9xec0 arabidopsis
78	28	100.0	1015	Q4F554_USTMA	Q4p554 ustilago ma
79	28	100.0	1112	Q7Q416_ANOGA	Q7q416 anopheles g
80	28	100.0	1222	VCIP1_HUMAN	Q96jh7 homo sapien
81	28	100.0	1232	Q504T4_HUMAN	Q504t4 homo sapien
82	28	100.0	1250	Q23409_CABEL	Q23409 caenorhabdi
83	28	100.0	1251	Q5WN33_CABER	Q5wn33 caenorhabdi
84	28	100.0	1697	Q5U928_9CALI	Q5u928 norovirus h
85	28	100.0	1699	POLN_LORDV	P54634 l non-etruc
86	28	100.0	1699	Q5XPY2_9CALI	Q5xpy2 norovirus h
87	28	100.0	1699	Q68103_9CALI	Q68103 hawaii cali
88	28	100.0	1699	Q6PPW2_9CALI	Q6ppw2 norovirus h
89	28	100.0	1699	Q6PPW5_9CALI	Q6ppw5 norovirus h
90	28	100.0	1699	Q6PPW8_9CALI	Q6ppw8 norovirus h
91	28	100.0	1699	Q6PPX1_9CALI	Q6ppx1 norovirus h
92	28	100.0	1699	Q6PPX4_9CALI	Q6ppx4 norovirus h
93	28	100.0	1699	Q6PPY7_9CALI	Q6ppy7 norovirus h
94	28	100.0	1699	Q6PPY0_9CALI	Q6ppy0 norovirus h
95	28	100.0	1699	Q6PT65_9CALI	Q6pt65 human calic
96	28	100.0	1699	Q6REV3_9CALI	Q6rev3 norovirus g
97	28	100.0	1699	Q6REW2_9CALI	Q6rew2 norovirus g
98	28	100.0	1699	Q6RYF7_9CALI	Q6ryf7 human calic
99	28	100.0	1699	Q76MP6_9CALI	Q76mp6 norwalk-lik
100	28	100.0	1699	Q80RD7_9CALI	Q80rd7 snow mounta

ALIGNMENTS

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RESULT 1
Q84247 ORYSA PRELIMINARY; PRT; 70 AA.
AC Q84247
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein P0458G06.105 (Hypothetical protein
OS OSJNB0039C01.142)
DE Name=P0458G06.105; Synonyms=OSJNB0039C01.142;
GN Oryza sativa (japonica cultivar-group)
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Echaritidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0458G06.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0039C01.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005051; BAC57333.1; -; Genomic DNA.
DR EMBL; AP005768; BAD31689.1; -; Genomic DNA.
DR Gramene; Q84247; -.
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7281 MW; FE752CC92EB2B855 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 34 DYGMS 38

RESULT 2
Q9HCC1 HUMAN PRELIMINARY; PRT; 112 AA.
AC Q9HCC1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -; mRNA.
DR HSSP; P01783; 1IGC.
DR SMC; Q9HCC1; 1-112.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 112;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 31 DYGMS 35

RESULT 3
Q4W515 CAEL PRELIMINARY; PRT; 122 AA.
AC Q4W515
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORPNames=P42G2.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF024499; AAY5833.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 122 AA; 13287 MW; EC3A8B6FEFF859C CRC64;

Query Match 100.0%; Score 28; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
DB 69 DYGMS 73

RESULT 4
Q726K5 DESVH PRELIMINARY; PRT; 195 AA.
AC Q726K5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DVU3102;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1507118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolony J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Dougherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Daviden T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough."
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AB017319; AAS97573.1; -; Genomic DNA.
DR TIGR; DVU3102; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
```

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DR GO; GO:0008565; P:protein transporter activity; IEA.
DR CO; CO:0015031; P:protein transport; IEA.
DR InterPro; IPR006260; TonB_C.
DR TIGRFAMs; TIGR01352; tonB_Cterm; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 195 AA; 19904 MW; DF156A576C05C412 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMS 5
Db 82 DYGMS 86

RESULT 5
O08823 MOUSE
ID O08823_MOUSE PRELIMINARY; PRT; 204 AA.
AC O08823;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Axonemal dynein heavy chain (Fragment).
CN Name=Dnahc7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Testis;
RX MEDLINE=9803892; PubMed=9373155; DOI=10.1016/S0378-1119(97)00417-4;
RA Neesen J., Koehle M., Kirschne R., Steinlein C., Kreutzberger J.,
RA Engel W., Schmid M.;
RT "Identification of dynein heavy chain genes expressed in human and
RT mouse testis: chromosomal localization of an axonemal dynein gene.";
RL Gene 200:193-202(1997).
DR EMBL; Z83813; CAB06067.1; -; mRNA.
DR Ensembl; ENSMUSG0000046254; Mus musculus.
DR MGI; MGI:107731; Dnahc2.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22449 MW; 9AFFDA82E4603746 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMS 5
Db 199 DYGMS 203

RESULT 7
Q69K89 ORYSA
ID Q69K89_ORYSA PRELIMINARY; PRT; 206 AA.
AC Q69K89;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNB0079K11.23.
CN Name=OSJNB0079K11.23;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
RT clone:OSJNB0079K11.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005971; BAD36615.1; -; Genomic_DNA.
DR Gramene; Q69K89; -;
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 23255 MW; 9628AC2F986F43D2 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMS 5
Db 120 DYGMS 124

RESULT 8
Q57G17 SALCH
ID Q57G17_SALCH PRELIMINARY; PRT; 227 AA.
AC Q57G17;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Putative fimbrial chaparrone protein.
CN Name=stha; OrderedLocustNames=SC4439;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
DR EMBL: AE017220; AAX68345.1; -; Genomic DNA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0007047; P:cell wall organization and biogenesis; IEA.
DR InterPro: IPR001829; Pili_chaperone.
DR Pfam: PF02753; Pili_assembly_C; 1.
DR Pfam: PF00345; Pili_assembly_N; 1.
DR PRINTS: PR00969; CHAPERONPILI.
DR PROSITE: PS00635; PILI_CHAPERONE; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 227 AA; 24801 MW; B7F55939A55CFA37 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 215 DYGMS 219

RESULT 9
QSPNA2 SALPA
ID QSPNA2 SALPA PRELIMINARY; PRT; 227 AA.
AC QSPNA2;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DE Putative fimbrial chaperone protein.
GN Name=sthB; OrderedLocusNames=SPA4404;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 9150 / SAR842;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
DR EMBL: CP000026; AAV60127.1; -; Genomic DNA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0007047; P:cell wall organization and biogenesis; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR001829; Pili_chaperone.
DR Pfam: PF02753; Pili_assembly_C; 1.
DR Pfam: PF00345; Pili_assembly_N; 1.
DR PRINTS: PR00969; CHAPERONPILI.
DR PRODOM: PD001447; Pili_chaperone; 1.
DR PROSITE: PS00635; PILI_CHAPERONE; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 227 AA; 24799 MW; 6BA826626A26BD95 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 215 DYGMS 219

RESULT 10
Q8Z0S8 SALT
ID Q8Z0S8 SALT PRELIMINARY; PRT; 227 AA.
AC Q8Z0S8; Q7C455;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE Putative fimbrial chaperone protein.
GN Name=sthB; OrderedLocusNames=STV4943, t4633;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL: AL627284; CAD03425.1; -; Genomic DNA.
DR EMBL: AE016849; AA072062.1; -; Genomic_DNA.
DR HSP; P28926; IP5U.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0007047; P:cell wall organization and biogenesis; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR001829; Pili_chaperone.
DR Pfam: PF02753; Pili_assembly_C; 1.
DR Pfam: PF00345; Pili_assembly_N; 1.
DR PRINTS: PR00969; CHAPERONPILI.
DR PRODOM: PD001447; Pili_chaperone; 1.
DR PROSITE: PS00635; PILI_CHAPERONE; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 227 AA; 24829 MW; 6E8F92D7B5421AD1 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 215 DYGMS 219

RESULT 11
Q8ZJU0 SALT
ID Q8ZJU0 SALT PRELIMINARY; PRT; 227 AA.
AC Q8ZJU0;
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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative fibrial chaparone protein.
 GN Name=stha; OrderedLocusNames=STM4594;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewe N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AS008916; AAL23409.1; -; Genomic DNA.
 DR HSP; P26926; 1P5U.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0007047; P:cell wall organization and biogenesis; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPRO01829; Pili_chaperone.
 DR Pfam; PF02753; Pili_assembly_C; 1.
 DR Pfam; PF00345; Pili_assembly_N; 1.
 DR PRINTS; PR00969; CHAPERONPILI.
 DR Prodom; PD001447; Pili_chaperone; 1.
 DR PROSITE; PS00635; PILI_CHAPERONE; 1.
 DR Chaperone; Complete proteome.
 SK SEQUENCE 227 AA; 24743 MW; EC0D30D9487CD7DF CRC64;

Query Match 100.0%; Score 28; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMs 5
 Db 215 DYGMs 219

RESULT 12
 Q6GR19 XENLA
 ID Q6GR19_XENLA PRELIMINARY; PRT; 242 AA.
 AC Q6GR19_2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC81350 protein.
 GN Name=MGC81350;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC071115; AAT71115.1; -; mRNA.
 SQ SEQUENCE 242 AA; 27476 MW; 203357CE8C1AEB09 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
 Db 35 DYGMs 39

RESULT 13
 Q6E260 ARATH
 ID Q6E260_ARATH PRELIMINARY; PRT; 245 AA.
 AC Q6E260;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AC396710;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Xiao Y., Underwood B., Moskal W., Torian U., Redman J., Wu H.C.,
 RA Utterback T., Town C.D.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
 RA Wu H.C., Utterback T., Town C.D.;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY600563; AAT68362.1; -; mRNA.
 DR EMBL; AY773873; AAV63902.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 245 AA; 27802 MW; 43C5412313106ABB CRC64;

Query Match 100.0%; Score 28; DB 2; Length 245;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMs 5
 Db 40 DYGMs 44

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RESULT 14
Q6NU71 XENLA
ID Q6NU71 XENLA PRELIMINARY; PRT; 246 AA.
AC Q6NU71
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MG81187 protein.
GN Name=MGC81187;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywicki M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC068729; AAH68729.1; -, mRNA.
DR GO; GO:0003676; P:nuclear acid binding; IEA.
DR GO; GO:0000398; P:nuclear mRNA splicing, via spliceosome; IEA.
DR InterPro; IPR012677; a_b_plait_nuc_bd.
DR InterPro; IPR000504; RNP1_RNA_Ed.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 246 AA; 27984 MW; 59F317B368FD6825 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGM5 5
Db 111 DYGM5 115

, RESULT 15

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Q8E110_STRAS
ID Q8E110_STRAS PRELIMINARY; PRT; 249 AA.
AC Q8E110;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Prophage LambdaSal, antirepressor, putative.
GN OrderedLocuNames=SAG0555;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=216466;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mota M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.B., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL; AE014217; AAM99456.1; -, Genomic_DNA.
DR TIGR; SAG0555; -.
KW Complete proteome.
SQ SEQUENCE 249 AA; 29176 MW; F6537740D2C89258 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGM5 5
Db 163 DYGM5 167

RESULT 16
Q6GM50 XENLA
ID Q6GM50 XENLA PRELIMINARY; PRT; 255 AA.
AC Q6GM50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC83967 protein.
GN Name=MGC83967;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074235; AAH74235.1; -; mRNA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000398; P:nuclear mRNA splicing, via spliceosome; IEA.
DR InterPro; IPR012677; a_b_plait_nuc_bd.
DR InterPro; IPR000504; RNP1_RNA_bd.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
SQ SEQUENCE 255 AA; 29100 MW; 16D6083A5F8D85 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 111 DYGMS 115

RESULT 17
QAKT14 9NUCL
ID QAKT14 9NUCL PRELIMINARY; PRT; 263 AA.
AC QAKT14;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE PCNA
GN Name=ORF-66 pcna;
OS Chrysoideixis chalcites nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=320432;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15567439; DOI=10.1016/j.virol.2004.09.032;
RA van Oers M.M., Herniou E.A., Umany M., Messelink G.J., Vlak J.M.;
RT "Identification and characterization of a DNA photolyase-containing
baculovirus from Chrysoideixis chalcites.";
RL Virology 330:460-470 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15958686; DOI=10.1099/vir.0.80964-0;
RA van Oers M.M., Abma-Henkens M.H.C., Herniou E.A., de Groot J.C.W.,
RA Peters S., Vlak J.M.;
RT "Genome sequence of Chrysoideixis chalcites nucleopolyhedrovirus, a
baculovirus with two DNA photolyase genes.";
RL J. Gen. Virol. 86:2069-2080 (2005).
DR EMBL; AY864330; AY83997.1; -; Genomic DNA.
SQ SEQUENCE 263 AA; 30207 MW; AEDFC28F9B5C275F CRC64;

Query Match 100.0%; Score 28; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 125 DYGMS 129

RESULT 18
WOX13 ARATH
ID WOX13 ARATH STANDARD; PRT; 268 AA.
AC O81788;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE WUSCHEL-related homeobox 13.
GN Name=WOX13; OrderedLocNames=At4g35550; ORFNames=F8D20.60;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=cv. Landsberg erecta;
RX PubMed=14711878; DOI=10.1242/dev.00963;
RA Haecker A., Gross-Hardt R., Geiges B., Sarkar A., Breuninger H.,
RA Herrmann M., Laux T.;
RA "Expression dynamics of WOX genes mark cell fate decisions during
early embryonic patterning in Arabidopsis thaliana.";
RL Development 131:657-668 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198; DOI=10.1038/47134;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Medler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens J., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramepger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Berger C., Schmidt W., Lecharny A., Aubourg S.,
RA Chedof F., Cooke R., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dente M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

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RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RL thaliana.";
RL Nature 402:769-777(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=cv. Columbia.
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari P.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju N., Goldsmith A.D., Gurjal M., Hansen N.P.,
RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tanase R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RL genome.";
RL Science 302:842-846(2003).
CC -1- FUNCTION: Transcription factor which may be involved in
CC developmental processes (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the WUS homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox DNA-binding domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY2511404; AAP37142.1; -; mRNA.
DR EMBL; AL031135; CAA20025.1; -; Genomic DNA.
DR EMBL; AL161587; CAB80271.1; -; Genomic DNA.
DR EMBL; AY048268; AAK82530.1; -; mRNA.
DR EMBL; BT000538; AAN18107.1; -; mRNA.
DR PIR; T04660; T04660.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR012287; Homeobox domain-rel.
DR Pfam; PF00046; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; FALSE_NEG.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
KW Transcription; transcription regulation.
FT DNA BIND 95 159 Homeobox; WUS-type.
SQ SEQUENCE 268 AA; 29673 MW; D57FCC13AB1A93DA CRC64;

Query Match 100.0%; Score 28; DB 1; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 263 DYGMS 267

RESULT 19
Q9SKM6 ARATH PRELIMINARY; PRT; 268 AA.
AC Q9SKM6 ARATH
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE En/Spm-like transposon protein (proline-rich family protein).
```

```
GN ORFNames=At3g28440;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Sheu T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Utterback T., Town C.D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006283; AAD20682.1; -; Genomic DNA.
DR EMBL; DQ056548; AAY78699.1; -; mRNA.
DR PIR; H84684; H84684.
SQ SEQUENCE 268 AA; 27741 MW; 0584FDE4622FED0E CRC64;

Query Match 100.0%; Score 28; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 218 DYGMS 222

RESULT 20
Q742X5 MYCPA
ID Q742X5 MYCPA PRELIMINARY; PRT; 280 AA.
AC Q742X5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=MAP0710C;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
DR EMBL; AE017229; AAS03027.1; -; Genomic DNA.
DR HSP; P47227; IBD.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002347; Adh_short_C2.
DR InterPro; IPR002424; Insect adh_fam.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PRO0081; GDRDH.
DR PRINTS; PRO1167; INSADHFAMILY.
DR PROSITE; PS00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 280 AA; 29737 MW; 168F11C6F2D9DD51 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 280;
```

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 DYGMS 5
Db 208 DYGMS 212

RESULT 21
Q8PFO XANAC PRELIMINARY; PRT; 293 AA.
ID Q8PFO XANAC PRELIMINARY;
AC Q8PFO;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Hypothetical protein XAC3950.
GN OrderedLocusNames=XAC3950;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Ciapina L.E.A., Camarotte G., Cannavan F., Cardozo J., Chamberg F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Borhy H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoza L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AS012044; AM38787.1; -: Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 3315 MW; 8CAC3C831EA0B33F CRC64;

Query Match 100.0%; Score 28; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 DYGMS 5
Db 234 DYGMS 238

RESULT 22
Q9C840 ARATH PRELIMINARY; PRT; 300 AA.
ID Q9C840 ARATH PRELIMINARY;
AC Q9C840;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein T8E24.2.
GN Name=T8E24.2;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidops.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC036106; AAG51001.1; -: Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 33773 MW; C05A46267AFCE3F4 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 DYGMS 5
Db 32 DYGMS 36

RESULT 23
Q9M7X8 ARATH PRELIMINARY; PRT; 302 AA.
ID Q9M7X8 ARATH PRELIMINARY;
AC Q9M7X8;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE F3E22.15 protein.
GN Name=F3E22.15;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC023912; AAF63827.1; -: Genomic DNA.
SQ SEQUENCE 302 AA; 34042 MW; C7C97F75F2825AE9 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 4.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 DYGMS 5
Db 32 DYGMS 36

RESULT 24
Q54KM8 DICDI PRELIMINARY; PRT; 323 AA.
ID Q54KM8 DICDI PRELIMINARY;
AC Q54KM8;
DT 13-SEP-2005 (TREMELrel. 31, Created)
DT 13-SEP-2005 (TREMELrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMELrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD0187382;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugeng R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

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RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louissegh H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauleky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
RA "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0-0(2005).
CC -!- EMBL/GenBank/DDA whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF101000149; EAL6320.1; -; Genomic_DNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004672; P:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
KW Hypothetical protein; Nucleotide-binding.
SQ SEQUENCE 323 AA; 37891 MW; 9D6AA77877060CE4 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 189 DYGMS 193

RESULT 25
Q4JAU3 SULAC
ID Q4JAU3 SULAC PRELIMINARY; PRT; 333 AA.
AC Q4JAU3
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Conserved Archaeal protein.
GN OrderedLocusNames=Saci_0707;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RX PubMed=15995215; DOI=10.1128/JB.187.14.4992-4999.2005;
RA Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
RA Grave B., Awayez M., Zibat A., Klien H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
RT Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AAY80086.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 333 AA; 37526 MW; B431416E3C186257 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 245 DYGMS 249

RESULT 26
Q6L162 PICTO
ID Q6L162_PICTO PRELIMINARY; PRT; 333 AA.

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AC Q6L162;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Oligopeptide ABC transporter Dpp2, permease protein.
GN OrderedLocusNames=PT00705;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT43290.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp_1; 1.
KW Complete proteome.
SQ SEQUENCE 333 AA; 37930 MW; 69C2A83E8B763DCA CRC64;
Query Match 100.0%; Score 28; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGMS 5
Db 235 DYGMS 239

RESULT 27
OTCC RHIME
ID OTCC RHIME STANDARD; PRT; 334 AA.
AC Q2ZTL;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase).
GN Name=arCB, OrderedLocusNames=RA0368; ORFNames=SMA0695;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA (megaplasmid 1).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=1021;
RX MEDLINE=21336509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation; arginine deiminase pathway; second
CC step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the ATCase/OTCase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----
 CC EMBL; AE007228; AAK65026.1; -; Genomic_DNA.
 CC DR PIR; H95307; H95307.
 CC DR HSP; P08308; 1DXH.
 CC DR HAMAP; MF_01109; -; 1.
 CC DR InterPro; IPR006130; Asp/Omn Cotranf.
 CC DR InterPro; IPR006131; Asp Orn bd.
 CC DR InterPro; IPR006132; OCTace_P bd.
 CC DR InterPro; IPR002292; Orn carbamyltrans.
 CC DR Pfam; PF00185; OCTace; 1.
 CC DR Pfam; PF02729; OCTace_N; 1.
 CC DR PIRSF; PIRSF000416; OCT_ATCase; 1.
 CC DR PRINTS; PRO0100; AOTCASE.
 CC DR PRINTS; PRO0102; OCTCASE.
 CC DR TIGRFAMs; TIGR00658; orn carb tr; 1.
 CC DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
 CC KW Arginine metabolism; Complete proteome; Plasmid; Transferase.
 CC FT SITE 32 32 Important for structural integrity (By
 CC similarity).
 CC FT SITE 57 61 Carbamoylphosphate binding (By
 CC similarity).
 CC FT SITE 108 108 Carbamoylphosphate binding (By
 CC similarity).
 CC FT SITE 135 135 Carbamoylphosphate binding (By
 CC similarity).
 CC FT SITE 148 148 Important for structural integrity (By
 CC similarity).
 CC FT SITE 273 276 Ornithine binding (By similarity).
 CC FT SITE 334 AA; 37660 MW; BD7A703ABDB63DAE CRC64;
 CC SQ SEQUENCE 334 AA; 37660 MW; BD7A703ABDB63DAE CRC64;

Query Match 100.0%; Score 28; DB 1; Length 334;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 DB 292 DYGMS 296

RESULT 28
 Q9YDP1 AERPE PRELIMINARY; PRT; 340 AA.
 ID Q9YDP1;
 AC Q9YDP1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE0874.
 GN OrderedLocusNames=APE0874;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 CC NCBI_TaxID=56636;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 RL EMBL; BA000002; BAA79856.1; -; Genomic_DNA.
 DR PIR; H72681; H72681.
 DR Complete proteome; Hypothetical protein.
 KW SEQUENCE 340 AA; 39481 MW; 369F8FA81963C3EF CRC64;

Query Match 100.0%; Score 28; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 DB 82 DYGMS 86

RESULT 29
 QANRK8 9DELT PRELIMINARY; PRT; 342 AA.
 ID Q4NRK8 9DELT PRELIMINARY; PRT; 342 AA.
 AC Q4NRK8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Peptidase M41.
 GN ORFNames=AdenDRAFT_1374;
 OS Anaeromyxobacter dehalogenans 2CP-C.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cytophactereae; Myxococaceae; Anaeromyxobacter.
 CC NCBI_TaxID=290397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pittluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; AAHD01000026; EAL78259.1; -; Genomic DNA.
 SQ SEQUENCE 342 AA; 37312 MW; 6A27B92CA156FE01 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 342;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5
 DB 198 DYGMS 202

RESULT 30
 Q4HT34 CAMUP PRELIMINARY; PRT; 350 AA.
 ID Q4HT34 CAMUP PRELIMINARY; PRT; 350 AA.
 AC Q4HT34;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Branched chain amino acid ABC transporter, permease protein.
 GN Names=liiVM; ORFNames=CUP0847;
 OS Campylobacter upsaliensis RM3195.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 CC NCBI_TaxID=306264;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM3195;
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,

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RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.B.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DSC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFJ01000001; EAL54085.1; -; Genomic DNA.
SQ SEQUENCE 350 AA; 38157 MW; 0DA5BE266687DA2B CRC64;

Query Match 100.0%; Score 28; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 29 DYGMS 33

RESULT 31
Q4IEG8 GIBZE PRELIMINARY; PRT; 352 AA.
AC Q4IEG8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=FG04390.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
OC Hypocotycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeAtellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gagdyna S., Gnerre S., Graham L., Grand-Pierre N., Harez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasany U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000190; EAA72771.1; -; Genomic DNA.
SQ SEQUENCE 352 AA; 36014 MW; AF380E4B072DC933 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 29 DYGMS 33

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Db 342 DYGMS 346

RESULT 32
Q5MD63 BOVIN PRELIMINARY; PRT; 352 AA.
AC Q5MD63;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Chemokine receptor 5.
GN Name=CCR5;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Blumberman S.L., Baldwin C.L.;
RT "Molecular cloning and characterization of bovine chemokine
RT receptors.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AY834252; AAV97929.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chklike_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 40144 MW; FEBDF387906561C7 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
Db 13 DYGMS 17

RESULT 33
Q6YT41 PIG PRELIMINARY; PRT; 352 AA.
AC Q6YT41;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Chemokine (C-C motif) receptor 5 (Chemokine C-C motif eceptor 5).
GN Name=CCR5;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 RL Uenishi H.;
 RN "Genomic structure of eight porcine chemokine receptors and intergene
 sharing of an exon between CCR1 and XCR1.";
 RL Gene 349:55-66(2005).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC EMBL; AF006185; BAD08649.1; -; Genomic DNA.
 DR EMBL; AF006435; BAD08656.1; -; Genomic DNA.
 DR EMBL; AB119272; BAD12135.1; -; mRNA.
 DR GO; GO:0016021; C-integral to membrane; IEA.
 DR GO; GO:0016493; F-C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F-receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P-signal transduction; IEA.
 DR InterPro; IPR002240; CC_5 receptor.
 DR InterPro; IPR000355; ChkMkin_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 KW G-PROTEIN COUPLED RECEPTOR
 SQ SEQUENCE 352 AA; 40228 MW; 7464CB930911C987 CRC64;
 Query Match 100.0%; Score 28; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYGMS 5
 Db 13 DYGMS 17
 RESULT 34
 CCR5_MOUSE STANDARD; PRT; 354 AA.
 ID CCR5_MOUSE STANDARD; PRT; 354 AA.
 AC F5182; O35313; O35891; P97308; P97405; Q61867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
 alpha receptor).
 DE Names=CCR5; Synonyms=Cmkbr5;
 OS Mus musculus (Mouse).
 GN Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SvJ; TISSUE=Spleen;
 RX MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
 RA Boring L., Goelling J., Montecarlo F.S., Luis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RN "Molecular cloning and functional expression of murine JE (monocyte
 chemoattractant protein 1) and murine macrophage inflammatory protein
 1alpha receptors: evidence for two closely linked C-C chemokine
 receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445;
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Cloning and characterization of a novel murine macrophage
 inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 271:14445-14451 (1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/Ola;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 implicate specific amino acids in infections by simian and human
 immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656 (1997).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharon M., Cen Y.H.,
 Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314 (1997).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 but not in nonhematopoietic cell lines.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC EMBL; U47036; AAC52454.1; -; mRNA.
 DR EMBL; X94151; CAA63867.1; -; mRNA.
 DR EMBL; U68565; AAB37273.1; -; Genomic DNA.
 DR EMBL; U83327; AAC53386.1; -; Genomic DNA.
 DR EMBL; AF022990; AAC53389.1; -; Genomic DNA.
 DR EMBL; AF019772; AAB71183.1; -; Genomic DNA.
 DR EMBL; D83648; BAA12024.1; -; mRNA.
 DR Ensembl; ENSMUSG00000035359; Mus musculus.
 DR MGI; MGI:107182; Ccr5.
 DR GO; GO:0016021; C-integral to membrane; TAS.
 DR GO; GO:0016493; F-C-C chemokine receptor activity; IEA.
 DR GO; GO:0006952; P-defense response; IMP.
 DR InterPro; IPR002240; CC_5 receptor.
 DR InterPro; IPR000355; ChkMkin_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Receptor;
KW Transducer; Transmembrane.
FT TOPO_DOM 1 32 Extracellular (Potential).
FT TRANSMEM 33 60 1 (Potential).
FT TOPO_DOM 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 2 (Potential).
FT TOPO_DOM 92 104 Extracellular (Potential).
FT TRANSMEM 105 126 3 (Potential).
FT TOPO_DOM 127 143 Cytoplasmic (Potential).
FT TRANSMEM 144 168 4 (Potential).
FT TOPO_DOM 169 200 Extracellular (Potential).
FT TRANSMEM 201 220 5 (Potential).
FT TOPO_DOM 221 237 Cytoplasmic (Potential).
FT TRANSMEM 238 262 6 (Potential).
FT TOPO_DOM 263 279 Extracellular (Potential).
FT TRANSMEM 280 303 7 (Potential).
FT TOPO_DOM 304 354 Cytoplasmic (Potential).
FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
FT DISULFID 103 180 By similarity.
FT VARIANT 11 11 I -> S.
FT VARIANT 62 62 K -> R.
FT VARIANT 66 66 V -> M.
FT VARIANT 97 97 I -> V.
FT VARIANT 109 109 V -> L.
FT VARIANT 156 156 V -> A.
FT VARIANT 160 160 F -> S.
FT VARIANT 185 185 P -> L.
FT VARIANT 213 213 I -> V.
FT VARIANT 318 318 H -> Y (in Ref. 3).
FT VARIANT 337 337 P -> S (in Ref. 1).
FT CONFLICT 3 3 F -> L (in Ref. 2).
FT CONFLICT 80 80 L -> P (in Ref. 2).
FT CONFLICT 145 145 N -> I (in Ref. 5).
FT CONFLICT 190 190 H -> Y (in Ref. 3).
FT CONFLICT 208 208 P -> S (in Ref. 1).
SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;
Query Match 100.0%; Score 28; DB 1; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGM5 5
Db 15 DYGM5 19
RESULT 35
Q5RIS0 MOUSE PRELIMINARY; PRT; 354 AA.
AC Q5RIS0
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein.
GN Name=OTTMUSP0000001218; ORFNames=RP23-289L21.1-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA North P., Leaves N., Graystrong J., Coppola M., Manjunath S.,
RA Russell E., Smith M., Strachan G., Tofts C., Boal E., Cobley V.,
RA Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
RA Botcherby M.R.M.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX247953; CAI24944.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 354 AA; 40845 MW; 3D3800569BBEA152 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGM5 5
Db 15 DYGM5 19
RESULT 36
Q7CCF5_ECOL6 PRELIMINARY; PRT; 361 AA.
AC Q7CCF5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein c3559.
GN OrderedLocNames=c3559;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raako D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AB016766; AAN82007.1; -; Genomic DNA.
DR GO; GO:0008484; P:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
KW Complete proteome.
SQ SEQUENCE 361 AA; 40334 MW; EF1B8D796D56DA52 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DYGM5 5
Db 251 DYGM5 255
RESULT 37
Q9LTC3_ARATH PRELIMINARY; PRT; 362 AA.
ID Q9LTC3_ARATH
AC Q9LTC3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gb|AAC62811.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty P1 and TAC
clones.";
RL DNA Res. 7:131-135 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025608; BAA95739.1; -, Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006527; F_box_assoc_1.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF07734; FBA_1; 1.
DR SMART; SM00256; FBOX; 1.
DR TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 362 AA; 41908 MW; A34137F0420A53EC CRC64;

Query Match 100.0%; Score 28; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 5.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 DYGMS 5

|||||

300 DYGMS 304

RESULT 38

Q9EYS9_9RHIZ PRELIMINARY; PRT; 406 AA.

AC Q9EYS9; 1

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Mimosine amino transferase.

GN Name=midD;

OS Rhizobium sp. TAL1145.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.

OX NCBI_TaxID=147233;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=TAL1145;

RX MEDLINE=22511528; PubMed=12624215; DOI=10.1099/mic.0.25954-0;

RA Borthakur D., Soedarto M., Fox P.M., Webb D.T.;

RT "The mid genes of Rhizobium sp strain TAL1145 are required for

RT degradation of mimosine into 3-hydroxy-4-pyridone and are inducible by

RT mimosine.";

RL Microbiology 149:537-546(2003).

DR EMBL; AF312768; AAG47972.2; -, Genomic_DNA.

DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.

DR GO; GO:0008483; F:transaminase activity; IEA.

DR GO; GO:0009058; P:biosynthesis; IEA.

DR InterPro; IPR001176; ACC synthase.

DR InterPro; IPR004839; Aminotrans_I/II.

DR Pfam; PF00155; Aminotran_1_2; 1.

DR PRINTS; PR00753; ACCSYNTHASE.

DR Transference.

QY SEQUENCE 406 AA; 45901 MW; ED94EC28E6CB24 CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 406;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

345 DYGMS 349

RESULT 39

P72895_SVNY3

ID P72895_SVNY3 PRELIMINARY; PRT; 411 AA.

AC P72895;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE S1r1617 protein.

GN OrderedLocusNames=s1r1617;

OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugiyama M., Saito M., Saito T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; BA000022; BAA16911.1; -, Genomic_DNA.
DR FIR; S74760; S74760.
DR SMR; P72895; 128-356.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 411 AA; 45405 MW; 1DE76566EB4D6533 CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 411;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYGMS 5

|||||

65 DYGMS 69

RESULT 40

Q87T65_VIBPA

ID Q87T65_VIBPA PRELIMINARY; PRT; 439 AA.

AC Q87T65;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Putative glutamate-1-semialdehyde 2,1-aminomutase.

GN OrderedLocusNames=VP0205;

OS Vibrio parahaemolyticus

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=670;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIT DNA].

RC STRAIN=RIMD 2210633 / Serotype O3:K6;

RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tegomori K.,

RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

RT distinct from that of V. cholerae.";

RL Lancet 361:743-749(2003).

CC -!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent

CC aminotransferase family.

DR EMBL; BA000031; BAC58468.1; -, Genomic_DNA.

DR HSSP; P24630; 4GSA.

DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.

DR GO; GO:0008483; F:transaminase activity; IEA.

DR InterPro; IPR005814; Aminotrans_3.

DR PANTHER; PTHR11986; Aminotrans_3; 1.

DR Pfam; PF00202; Aminotran_3; 2.

KW Complete proteome; Pyridoxal phosphate.

SQ SEQUENCE 439 AA; 48915 MW; FC9D51C98856A9E9 CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 439;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYGMS 5
|
|
|
|
Db 52 DYGMS 56

Search completed: November 18, 2005, 21:14:26
Job time : 72.8214 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:57:23 : Search time 217.357 Seconds
(without alignments)
34.365 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSGTGADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq 21.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	17	3	Aay95192 Anti-plat
2	96	100.0	17	5	Abg78240 Human Fv
3	96	100.0	17	5	Abg91931 Human ant
4	96	100.0	17	9	Adw77416 Human pla
5	96	100.0	17	9	Adw77404 Human pla
6	96	100.0	98	3	Aab40073 Anti-hi11
7	96	100.0	98	5	Abg78186 Human Fv
8	96	100.0	98	5	Abg91877 Human ant
9	96	100.0	98	6	Abg78087 Human ger
10	96	100.0	98	7	Adf09916 Antibody
11	96	100.0	98	7	Adf10126 Antibody
12	96	100.0	98	7	Adf10024 VEGF anti
13	96	100.0	98	7	Adj80300 VH gene 1
14	96	100.0	98	9	Ady75305 Protein e
15	96	100.0	113	3	Aay95177 Anti-plat
16	96	100.0	113	3	Aay95178 Anti-plat
17	96	100.0	113	3	Aay95189 Anti-plat
18	96	100.0	115	3	Aay95190 Anti-plat
19	96	100.0	116	2	Aaw19880 CEA-Speci
20	96	100.0	117	2	Aar66312 Human imm
21	96	100.0	117	9	Adx01783 SARS coro
22	96	100.0	118	4	Aau02560 Anti-adip
23	96	100.0	122	3	Aay96065 Human ant
24	96	100.0	123	8	Adj57861 Light var

25	96	100.0	207	5	AAU98019	Aau98019 Human ace
26	96	100.0	235	8	ADR28086	Adr28086 NPB polyp
27	96	100.0	238	3	AAy95198	Aay95198 Anti-plat
28	96	100.0	239	5	ABP46004	Abp46004 Human Bly
29	96	100.0	239	5	ABP46027	Abp46027 Human Bly
30	96	100.0	239	5	ABP44926	Abp44926 Human Bly
31	96	100.0	239	7	ADG95753	Adg95753 Single ch
32	96	100.0	239	7	ADG96854	Adg96854 Single ch
33	96	100.0	239	7	ADG96831	Adg96831 Single ch
34	96	100.0	242	7	ADG30497	Adg30497 Human GMC
35	96	100.0	242	8	ADI58068	Adi58068 Reg IV-sp
36	96	100.0	244	6	AAO31136	Aao31136 Human CM0
37	96	100.0	244	9	ADW90315	Adw90315 Phage scf
38	96	100.0	244	9	ADW90315	Adw90315 SARS coro
39	96	100.0	244	9	ADY34209	Ady34209 TRAIL rec
40	96	100.0	246	5	ABG78329	Abg78329 Human Fv
41	96	100.0	246	5	ABG92026	Abg92026 Antibody
42	96	100.0	249	7	ADG30407	Adg30407 Human GMB
43	96	100.0	256	5	ABG78334	Abg78334 Human Fv
44	96	100.0	256	5	ABG92025	Abg92025 Antibody
45	96	100.0	266	5	ABG92020	Abg92020 Human ant
46	96	100.0	277	5	ABG78150	Abg78150 Human Fv
47	96	100.0	277	5	ABG78328	Abg78328 Human Fv
48	96	100.0	277	5	ABG92019	Abg92019 Human ant
49	96	100.0	277	5	ABG91841	Abg91841 Human ant
50	96	100.0	277	8	ADS82026	Adi28366 Human pla
51	96	100.0	277	8	ADS82028	Adi28367 Human scf
52	96	100.0	278	8	ADI28367	Adi28367 Human scf
53	96	100.0	280	8	ADI28368	Adi28368 Human scf
54	96	100.0	280	8	ADJ57363	Adj57363 P-selecti
55	96	100.0	280	8	ADS82028	Adi28368 Human leu
56	96	100.0	280	8	ADT63078	Adt63078 Human scf
57	96	100.0	280	8	ADX01180	Adx01180 Amino aci
58	96	100.0	280	9	ADX01181	Adx01181 Amino aci
59	96	100.0	280	9	ADX01181	Adx01181 Amino aci
60	96	100.0	280	9	ADX01131	Adx01131 Amino aci
61	96	100.0	280	9	ADX01130	Adx01130 Amino aci
62	96	100.0	280	9	ADX01185	Adx01185 Amino aci
63	96	100.0	280	9	ADX01186	Adx01186 Amino aci
64	96	100.0	280	9	ADY78380	Ady78380 Single ch
65	96	100.0	280	9	ADY78325	Ady78325 Single ch
66	96	100.0	280	9	ADY78324	Ady78324 Single ch
67	96	100.0	280	9	ADY78379	Ady78379 Single ch
68	96	100.0	280	9	ADY78374	Ady78374 Single ch
69	96	100.0	280	9	ADY78375	Ady78375 Single ch
70	96	100.0	309	2	AAW83322	Aaw83322 Single ch
71	96	100.0	309	5	ABO96603	Abbo96603 Amino aci
72	96	100.0	309	6	ABG74384	Abg74384 Single ch
73	96	100.0	309	7	ADG98737	Adg98737 Human sin
74	96	100.0	309	8	ADO40446	Ado40446 Human sin
75	96	100.0	445	9	ADX02218	Adx02218 SARS coro
76	96	100.0	464	5	ABG78151	Abg78151 Human Fv
77	96	100.0	464	5	ABG91842	Abg91842 Human ant
78	93	96.9	126	5	AAU02603	Aau02603 Anti-adip
79	91	94.8	127	3	AAW52196	Aaw52196 Human ant
80	91	94.8	128	3	AAW52199	Aaw52199 Human ant
81	90	93.8	16	8	ADI28370	Adi28370 Human CDR
82	90	93.8	16	8	ADJ57365	Adj57365 p-selecti
83	90	93.8	16	8	ADS82030	Ads82030 Human scf
84	90	93.8	16	8	ADT63080	Adt63080 Human hyp
85	90	93.8	16	9	ADX01142	Adx01142 Cancer ce
86	90	93.8	17	9	ADY78336	Ady78336 Single ch
87	90	93.8	17	9	ADY26802	Ady26802 Human ant
88	90	93.8	17	9	AEA24209	Aea24209 Anti-HAHH
89	90	93.8	124	9	ADY26772	Ady26772 Anti-NGF
90	90	93.8	128	9	AEA24149	Aea24149 Anti-HAHH
91	90	93.8	263	5	AEA24175	Aea24175 Anti-HAHH
92	90	93.8	263	5	ABG92021	Abg92021 Antibody
93	82	85.4	494	3	ADQ65690	Adq65690 Novel hum
94	79	82.3	98	3	ABG40072	Abg40072 Anti-hi11
95	79	82.3	98	5	ABG78185	Abg78185 Human Fv
96	79	82.3	98	5	ABG91876	Abg91876 Human ant
97	79	82.3	99	3	AAV50960	Aay50960 Human FVI

XX Human antibody fragment #115.
 DE Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW stenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX Homo sapiens.
 OS WO200253700-A2.
 PN 11-JUL-2002.
 PD 31-DEC-2001; 2001WO-US049442.
 PF 29-DEC-2000; 2000US-00751181.
 PR 29-DEC-2000; 2000US-0258948P.
 XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
 PA Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
 PI WPI; 2002-674776/72.
 DR Novel isolated epitope present on cancer cells and important in
 PT physiological phenomena such as cell rolling, metastasis and
 PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 PT diseases, and cancer.
 PS Claim 25; Page 284-285; Opp; English.
 XX The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX
 XX Sequence 17 AA;
 Query Match 100.0%; Score 96; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GINWNGSGTGADSVK 17
 |||||
 Db 1 GINWNGSGTGADSVK 17
 |||||
 RESULT 4
 ADW77416
 ID ADW77416 standard; peptide; 17 AA.
 XX
 AC ADW77416;
 XX

DT 07-APR-2005 (first entry)
 XX Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 87.
 DE Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;
 KW Ophthalmological; Immunosuppressive; Vasotropic; Antibody;
 KW platelet membrane glycoprotein VI; diabetic retinopathy;
 KW cardiovascular disease; ocular disease; graft versus host disease;
 KW immune disorder.
 XX Homo sapiens.
 OS WO2005007800-A2.
 PN 27-JAN-2005.
 PD 20-JUL-2004; 2004WO-JP010596.
 PF 18-JUL-2003; 2003JP-00199192.
 PR (MOCH) MOCHIDA PHARM CO LTD.
 PA Takayama H, Shirakawa K, Yamakawa T, Kawahara T;
 PI WPI; 2005-152077/16.
 DR Novel human antibody or its active fragment capable of binding
 PT specifically with human platelet membrane glycoprotein VI and not
 PT inducing human platelet aggregation by itself, useful for treatment or
 PT prevention of thrombosis.
 XX Example 8; SEQ ID NO 87; 124pp; Japanese.
 XX The invention relates to a human antibody or its active fragment capable
 CC of binding specifically with human platelet membrane glycoprotein VI and
 CC not inducing human platelet aggregation by itself. The antibody is useful
 CC in treatment or prevention of thrombosis, embolism or arteriosclerosis.
 CC The antibody is useful in diagnosis of the disease by detecting or
 CC determining glycoprotein VI. The antibody is useful in the prevention
 CC and/or treatment of vascular endothelium failure, vascular endothelium
 CC hypertrophy, blood vessel restenosis, disseminated intravascular
 CC coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.
 CC The antibody exhibits high specificity with respect to glycoprotein VI,
 CC and can be obtained easily. The present sequence represents the amino
 CC acid sequence of a human platelet membrane glycoprotein VI associated
 CC CDR.
 XX Sequence 17 AA;
 Query Match 100.0%; Score 96; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GINWNGSGTGADSVK 17
 |||||
 Db 1 GINWNGSGTGADSVK 17
 |||||
 RESULT 5
 ADW77404
 ID ADW77404 standard; peptide; 17 AA.
 XX
 AC ADW77404;
 XX
 DT 07-APR-2005 (first entry)
 XX Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 75.
 DE Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;
 KW Ophthalmological; Immunosuppressive; Vasotropic; Antibody;
 KW platelet membrane glycoprotein VI; diabetic retinopathy;
 KW cardiovascular disease; ocular disease; graft versus host disease;
 KW immune disorder.

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XX OS Homo sapiens.
XX PN WO2005007800-A2.
XX XX
XX PD 27-JAN-2005.
XX XX
XX PF 20-JUL-2004; 2004WO-JP010596.
XX XX
XX PR 18-JUL-2003; 2003JP-00199192.
XX XX
XX PA (MOCH ) MOCHIDA PHARM CO LTD.
XX XX
XX PI Takayama H, Shirakawa K, Yamakawa T, Kawahara T;
XX XX
XX DR WPI; 2005-152077/16.
XX XX
XX PT Novel human antibody or its active fragment capable of binding
XX PT specifically with human platelet membrane glycoprotein VI and not
XX PT inducing human platelet aggregation by itself, useful for treatment or
XX PT prevention of thrombosis.
XX XX
XX PS Example 8; SEQ ID NO 75; 124pp; Japanese.
XX XX
XX CC The invention relates to a human antibody or its active fragment capable
XX CC of binding specifically with human platelet membrane glycoprotein VI and
XX CC not inducing human platelet aggregation by itself. The antibody is useful
XX CC in treatment or prevention of thrombosis, embolism or arteriosclerosis.
XX CC The antibody is useful in diagnosis of the disease by detecting or
XX CC determining glycoprotein VI. The antibody is useful in the prevention
XX CC and/or treatment of vascular endothelium failure, vascular endothelium
XX CC hypertrophy, blood vessel restenosis, disseminated intravascular
XX CC coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.
XX CC The antibody exhibits high specificity with respect to glycoprotein VI,
XX CC and can be obtained easily. The present sequence represents the amino
XX CC acid sequence of a human platelet membrane glycoprotein VI associated
XX CC CDR.
XX SQ
XX SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 96; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKVG 17
DB 1 GINWNGSGTGYADSVKVG 17
XX
RESULT 6
XX AAB40073
XX ID AAB40073 standard; protein; 98 AA.
XX AC
XX AC AAB40073;
XX XX
XX DT 05-FEB-2001 (first entry)
XX XX
XX DE Anti-hLL12 antibody H chain V region amino acid sequence SEQ ID 599.
XX XX
XX KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX KW complementarity determining region; CDR; antirheumatic; antiarthritic;
XX KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX KW multiple sclerosis; rheumatoid arthritis.
XX OS
XX OS Homo sapiens.
XX XX
XX PN WO200056772-A1.
XX XX
XX PD 28-SEP-2000.
XX XX
XX PF 24-MAR-2000; 2000WO-US007946.
XX XX
XX

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PR XX 25-MAR-1999; 99US-0126603P.
XX XX
XX PA (BADI ) BASF AG.
XX PA (GEMY ) GENETICS INST INC.
XX XX
XX PI Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;
XX PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
XX PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
XX PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
XX XX
XX DR WPI; 2000-638250/61.
XX XX
XX PT New human antibody specific for human interleukin-12 (IL-12) used to
XX PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
XX PT disease and multiple sclerosis.
XX XX
XX PS Claim 75; Page 121; 377pp; English.
XX XX
XX CC This invention relates to a new human antibody specific for human
XX CC interleukin-12 (IL-12). The invention also includes antigen binding
XX CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
XX CC anti-IL-12 antibody heavy and light chain complementarity determining
XX CC region (CDR) amino acid sequences, and also includes variable region
XX CC amino acid sequences. Other variable region amino acid sequences are
XX CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
XX CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
XX CC given in other CDR sequences. Light chain CDR3 consensus sequences are
XX CC given in AAB40064-B40067. Primers used in the identification and
XX CC construction of the antibodies of the invention are given in AAC61062-
XX CC C61071. The antibody of the invention is a neutralising antibody and has
XX CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
XX CC neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic;
XX CC antibacterial and immunosuppressive activity. The antibodies or antigen-
XX CC binding fragments are useful in the treatment of disorders associated
XX CC with detrimental release of human IL-12, especially Crohn's disease,
XX CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
XX CC manufacture of a pharmaceutical composition to treat human IL-12
XX CC disorders
XX XX
XX SQ Sequence 98 AA;
XX
Query Match 100.0%; Score 96; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKVG 17
DB 50 GINWNGSGTGYADSVKVG 66
XX
RESULT 7
XX ABG78186
XX ID ABG78186 standard; protein; 98 AA.
XX AC
XX AC ABG78186;
XX XX
XX DT 15-NOV-2002 (first entry)
XX XX
XX DE Human Fv molecule hypervariable region related peptide #61.
XX XX
XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX XX
XX OS Homo sapiens.
XX OS
XX PN WO200259264-A2.
XX XX
XX PD 01-AUG-2002.
XX XX
XX PF 31-DEC-2001; 2001WO-US049440.
XX XX
XX PR 29-DEC-2000; 2000US-00751181.
XX XX

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XX FA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
 XX PI Plaksin D, Peretz T;
 XX XX WPI; 2002-619166/66.
 XX DR
 XX XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
 XX PT or fragment, or construct of fragment with enhanced binding
 XX PT characteristics so as to selectively bind target cell in favor of other
 XX PT cells.
 XX XX
 XX PS Claim 13; Page 177-178; 232pp; English.
 XX CC The invention relates to a peptide or polypeptide comprising an Fv
 CC molecule, a construct or fragments or a construct of a fragment with
 CC enhanced binding characteristics which selectively and/or specifically
 CC binds to a target cell in favour of other cells, where binding is
 CC primarily determined by a first hypervariable region and Fv is a single
 CC chain Fv (scFv) or a disulfide Fv (darFv). The peptide, optionally in
 CC association with or attached, coupled, combined, linked or fused to a
 CC pharmaceutical agent, is useful in the manufacture of a medicament, where
 CC the medicament has activity against a diseased cell, preferably a cancer
 CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
 CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
 CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
 CC composition for use in inhibiting the growth of a diseased or cancer
 CC cell. This sequence represents a human Fv molecule hypervariable region
 CC related peptide of the invention
 XX CC
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 96; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GINWNGSGTGADSVKVG 17
 Db 50 GINWNGSGTGADSVKVG 66
 RESULT 8
 ABG91877
 ID ABG91877 standard; protein; 98 AA.
 XX AC ABG91877;
 XX XX
 XX DT 04-DEC-2002 (first entry)
 XX DE Human antibody fragment #61.
 XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
 KW metastasis; hypervariable region; autoimmune disease; thrombosis;
 KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
 KW myocardial infarction; retinopathic disease; abnormal platelet function;
 KW sulphated tyrosine-dependent protein-protein interaction.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN WO200253700-A2.
 XX XX
 XX PD 11-JUL-2002.
 XX XX
 XX PF 31-DEC-2001; 2001WO-US049442.
 XX XX
 XX PR 29-DEC-2000; 2000US-00751181.
 XX PR 29-DEC-2000; 2000US-0258948P.
 XX XX
 XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX XX
 XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
 PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX WPI; 2002-674776/72.
 XX DR
 XX XX Novel isolated epitope present on cancer cells and important in
 XX PT physiological phenomena such as cell rolling, metastasis and
 XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
 XX PT diseases, and cancer.
 XX XX
 XX PS Disclosure; Page 255; Opp; English.
 XX CC The invention relates to an isolated epitope present on cancer cells and
 CC important in physiological phenomena such as cell rolling, metastasis and
 CC inflammation, where the epitope is capable of being bound by an antibody,
 CC its antigen-binding fragment or its complex comprising at least one
 CC antibody or its binding fragment having a first hypervariable region. The
 CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
 CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
 CC tumour or leukaemia cells, increase in number of tumour or leukaemia
 CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
 CC platelet and/or cell-platelet adhesion or aggregation, for increasing
 CC mortality of tumour or leukaemia cells, for increasing the susceptibility
 CC of diseased cells to damage by anti-disease, anti-cancer or anti-
 CC leukaemia agents, or for decreasing the number of tumour or leukaemia
 CC cells in a patient, or in the manufacture of a medicament for the above
 CC mentioned purposes. The epitopes are useful for diagnosing and treating
 CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
 CC diseases, cardiovascular diseases such as myocardial infarction,
 CC retinopathic diseases and other diseases mediated by abnormal platelet
 CC function and diseases caused by sulphated tyrosine-dependent protein-
 CC protein interactions. This sequence represents a human antibody fragment
 CC of the invention
 XX CC
 XX SQ Sequence 98 AA;
 Query Match 100.0%; Score 96; DB 5; Length 98;
 Best Local Similarity 100.0%; Pred. No. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GINWNGSGTGADSVKVG 17
 Db 50 GINWNGSGTGADSVKVG 66
 RESULT 9
 ABO27087
 ID ABO27087 standard; protein; 98 AA.
 XX AC ABO27087;
 XX XX
 XX DT 10-SEP-2003 (first entry)
 XX DE Human germline heavy chain variable region gene segment #20.
 XX KW Human; heavy chain variable region; VH; humanised antibody;
 KW chimeric antibody; complementarity determining region; CDR;
 KW canonical CDR structure type.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN US2003039649-A1.
 XX XX
 XX PD 27-FEB-2003.
 XX XX
 XX PF 12-JUL-2002; 2002US-00194975.
 XX XX
 XX PR 12-JUL-2001; 2001US-0305111P.
 XX XX
 XX PA (FOOT/) FOOTE J.
 XX XX
 XX PI Foote J;
 XX XX
 XX DR WPI; 2003-492151/46.
 XX XX

PT Making humanized antibody for converting antibody, by making chimeric
 PT antibodies containing complementarity determining region from non-human
 PT antibody and appropriate framework sequences of human antibodies.
 XX
 XX
 PS Example 1; Fig 1; 31pp; English.
 PS
 XX The invention describes a method of making a humanised antibody,
 CC comprising making chimeric antibodies containing a complementarity
 CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human heavy chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. NO. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
 |||||
 Db 50 GINWNGSTGYADSVK 66

RESULT 10
 ADF09916
 ID ADF09916 standard; protein; 98 AA.

XX ADF09916;

XX 12-FEB-2004 (first entry)

XX Antibody heavy chain variable region VH_3-20.

XX Antibody; stability; solubility; antigen binding affinity;
 XX variable region; human.

XX Homo sapiens.

XX WO2003074679-A2.

XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
 PT comprises analyzing the interactions of amino acids at variable
 PT positions.

PS Disclosure; Fig 2a; 135pp; English.

XX The present invention relates to a method for optimizing at least one
 CC physico-chemical property of an antibody by a computational screening
 CC method. The method comprises: receiving a template antibody structure;
 CC selecting at least one variable position belonging to the antibody
 CC structure; selecting at least one amino acid to be considered at the
 CC variable position(s); analyzing the interaction of each selected amino
 CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one
 CC optimized physico-chemical property. The method is useful for optimizing
 CC the physico-chemical properties of an antibody, especially the stability,
 CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.

XX Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
 Best Local Similarity 100.0%; Pred. NO. 9.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
 |||||
 Db 50 GINWNGSTGYADSVK 66

RESULT 11

ADFI0126
 ID ADFI0126 standard; protein; 98 AA.

XX ADFI0126;

XX 12-FEB-2004 (first entry)

XX Antibody heavy chain variable region VH_3-20.

XX Antibody; stability; solubility; antigen binding affinity;
 XX variable region; human.

XX Homo sapiens.

XX WO2003074679-A2.

XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.

XX 01-MAR-2002; 2002US-0360843P.

XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.

XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
 PT comprises analyzing the interactions of amino acids at variable
 PT positions.

XX Example 16; Fig 40a; 135pp; English.

XX The present invention relates to a method for optimizing at least one
 CC physico-chemical property of an antibody by a computational screening
 CC method. The method comprises: receiving a template antibody structure;
 CC selecting at least one variable position belonging to the antibody
 CC structure; selecting at least one amino acid to be considered at the
 CC variable position(s); analyzing the interaction of each selected amino
 CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one

CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.

XX Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17
| | | | | | | | | | | | | | | | | | | | | |
Db 50 GINWNGSGTGYADSVK 66

RESULT 12

ADP10024
ID ADF10024 standard; protein; 98 AA.

XX AC ADF10024;

XX DT 12-FEB-2004 (first entry)

XX DE VEGF antibody heavy chain variable region VH_3-20.

XX KW Antibody; stability; solubility; antigen binding affinity;
XX KW variable region; human; VEGF.

XX OS Homo sapiens.

XX PN WO2003074679-A2.

XX PD 12-SEP-2003.

XX PF 03-MAR-2003; 2003WO-US006598.

XX PR 01-MAR-2002; 2002US-0360843P.

XX PR 29-MAY-2002; 2002US-0384197P.

XX PA (XENC-) XENCOR.

XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX DR WPI; 2003-722066/68.

XX PT Computer optimization of physicochemical properties of antibodies
XX PT comprises analyzing the interactions of amino acids at variable
XX PT positions.

XX PS Example 6; Fig 16a; 135pp; English.

XX CC The present invention relates to a method for optimizing at least one
XX CC physico-chemical property of an antibody by a computational screening
XX CC method. The method comprises: receiving a template antibody structure;
XX CC selecting at least one variable position belonging to the antibody
XX CC structure; selecting at least one amino acid to be considered at the
XX CC variable position(s); analyzing the interaction of each selected amino
XX CC acid at each variable position with at least part of the remainder of the
XX CC antibody, including the selected amino acids at other variable positions;
XX CC and identifying a set of at least one antibody sequence with at least one
XX CC optimized physico-chemical property. The method is useful for optimizing
XX CC the physico-chemical properties of an antibody, especially the stability,
XX CC solubility, or antigen binding affinity. The optimized antibody may be
XX CC useful for treating a patient. The present sequence is an antibody
XX CC variable region sequence used to illustrate the invention.

XX SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17
| | | | | | | | | | | | | | | | | | | | | |
Db 50 GINWNGSGTGYADSVK 66

RESULT 13

ADJ80300
ID ADJ80300 standard; protein; 98 AA.

XX AC ADJ80300;

XX DT 06-MAY-2004 (first entry)

XX DE VH gene locus antibody amino acid sequence #20.

XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.

XX OS Homo sapiens.

XX PN WO2003048321-A2.

XX PD 12-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038450.

XX PR 03-DEC-2001; 2001US-0336591P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Rother R, Wu D;

XX DR WPI; 2003-513753/48.

XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively
XX PT linking the selected framework sequences to one or more complementarity
XX PT determining regions of the initial antibody.

XX PS Disclosure; SEQ ID NO 60; 77pp; English.

XX CC The invention relates to a method of producing a hybrid antibody or
XX CC hybrid antibody fragment by: (i) providing an initial antibody having
XX CC specificity for a target; (ii) determining the sequence of a variable
XX CC region of the initial antibody; (iii) selecting a first component of the
XX CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
XX CC sequence of the first component to sequences contained in a reference
XX CC database of antibody sequences or antibody fragment sequences from a
XX CC target species; (v) selecting a sequence from an antibody in the database
XX CC which demonstrates a high degree of homology to the first component; (vi)
XX CC selecting a second component of the variable region which is different
XX CC than the first component, the second component selected from the group
XX CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
XX CC second component to sequences contained in a reference database of
XX CC antibody sequences or antibody fragment sequences from the target species
XX CC; (viii) selecting a sequence from the database which demonstrates a high
XX CC degree of homology to the second component and which is from a different
XX CC antibody than the selected antibody; and (ix) operatively linking the
XX CC selected framework sequences to one or more complementarity determining
XX CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
XX CC hybrid antibody fragment. The method is useful for producing a hybrid
XX CC antibody or hybrid antibody fragment (claimed). The antibody and
XX CC fragments are useful for therapeutic and diagnostic purposes. The method
XX CC uses entire framework regions from a single antibody variable heavy or
XX CC variable light chain to receive the CDRs. This produces antibodies that
XX CC are highly homologous and exhibit reduced immunogenicity while
XX CC maintaining an optimum binding profile. This sequence represents the
XX CC amino acid sequence of an antibody from the VH gene locus.

XX SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWGGSTGYADSVKG 17
|||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 14
ADY75305
ID ADY75305 standard; protein; 98 AA.

XX AC ADY75305;

XX DT 02-JUN-2005 (first entry)

XX DE Protein encoded by human germline heavy chain V minigene VH3 3-20.

XX KW Antibody engineering; antibody; antibody production; gene library;
KW DNA recombination; gene amplification; primer extension;
KW heavy chain variable region.

XX OS Homo sapiens.

XX PN WO2005023993-A2.

XX PD 17-MAR-2005.

XX PF 09-SEP-2004; 2004WO-US029617.

XX PR 09-SEP-2003; 2003US-0501073P.

XX PA (INTE-) INTEGRIGEN INC.

XX PI Sharma V, Leonard L, Smider V;

XX DR WPI; 2005-223364/23.

XX PT Producing polynucleotide encoding human germline antibody V-region for
PT generating full-length antibody germline V-region genes, by obtaining V
PT or J minigene and joining V minigene with J minigene, or joining J
PT minigene with V minigene.

XX PS Disclosure; Fig 10; 52pp; English.

XX CC The present invention relates to producing germline antibody genes by a
CC completely in vitro approach that mimics the natural process of V(D)J
CC recombination. The antibody genes are completely human and native in
CC their sequence, and libraries of such antibody genes can be constructed
CC which represent an unselected population representing the entire antibody
CC repertoire. The method uses gene amplification to produce a V minigene,
CC and a hybrid primer capable of hybridizing to a V minigene and either a D
CC or V minigene. The hybrid primer facilitates recombination of a V
CC minigene to a D or J minigene to produce a full length V-region gene.
CC Also disclosed is a library comprising member polynucleotides encoding
CC exogenously rearranged human germline antibody V-regions. In producing a
CC polynucleotide encoding a human germline antibody V-region, a D minigene
CC is further joined to the 3' end of the V minigene and the 5' end of the J
CC minigene. The V minigene or the J minigene in is obtained by chemical
CC synthesis or by amplification from a germline DNA library. Joining the V
CC minigene with at least one J minigene is performed by primer extension
CC using at least two or three oligonucleotide primers. The V minigene is
CC derived from human immunoglobulin kappa locus, human immunoglobulin
CC lambda locus, or human immunoglobulin heavy chain locus. The V-region
CC also comprises a serine protease triad. The human germline antibodies can
CC be used as precursors to more high affinity antibodies, and are useful in
CC the generation of efficiently pairing libraries of heavy and light
CC chains. The present sequence is a polypeptide encoded by human germline
CC heavy chain V minigene, family VH3 locus 3-20.

XX SQ Sequence 98 AA;

Query Match 100.0%; Score 96; DB 9; Length 98;

Best Local Similarity 100.0%; Pred. No. 9.3e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWGGSTGYADSVKG 17
|||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 15
AAY95177

ID AAY95177 standard; protein; 113 AA.

XX AC AAY95177;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human HIB-1 VH.

XX KW Variable heavy chain; single chain antibody; scFv; human; HIB-1;
KW Glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Region 1. .30
/note= "framework region 1"

FT Region 31. .34
/note= "complementarity determining region 1"

FT Region 35. .49
/note= "framework region 2"

FT Region 50. .86
/note= "complementarity determining region 2"

FT Region 67. .98
/note= "framework region 3"

FT Region 99. .104
/note= "complementarity determining region 3"

FT Region 105. .113
/note= "framework region 4"

XX WO200026667-A1.

XX PD 11-MAY-2000.

XX PF 29-OCT-1999; 99WO-US025495.

XX PR 30-OCT-1998; 98US-0106275P.

XX PA (MILL/) MILLER J L.

XX PI Miller JL;

XX DR WPI; 2000-365744/31.

XX DR N-PSDB; AAA27658.

XX CC Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
PT Ib alpha molecule useful for producing antibodies which inhibit platelet
PT aggregation.

XX PS Claim 10; Page 71; 89pp; English.

XX CC The present sequence is that of the heavy chain variable region (VH) of
CC human single chain antibody (scFv) HIB-1 (see AAY95198), which is
CC directed against platelet glycoprotein Ib (GPIb). The HIB series of scFv
CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of
CC phagemid selection against transfected CHO cells expressing the GPIb
CC alpha component of the GPIb/IX/V complex on their surface, followed by a
CC 4th round of selection against washed human platelets, and 2 final rounds
CC in which attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or mimotope peptide (see
CC AAY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences and
CC are therefore attractive potential reagents for therapeutic purposes.

CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIIb/IIIa and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed

XX Sequence 113 AA;

SQ Query Match 100.0%; Score 96; DB 3; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17
 DB 50 GINWNGSGTGYADSVK 66

RESULT 16

AA95178

ID AA95178 standard; protein; 113 AA.

XX AC AA95178;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human H1b-1 VH.

XX KW Variable heavy chain; single chain antibody; scFv; human; H1b-1;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..30 /note= "framework region 1"

FT Region 31..34 /note= "complementarity determining region 1"

FT Region 35..49 /note= "framework region 2"

FT Region 50..66 /note= "complementarity determining region 2"

FT Region 67..98 /note= "framework region 3"

FT Region 99..104 /note= "complementarity determining region 3"

FT Region 105..113 /note= "framework region 4"

FT WO200026667-A1.

FT 11-MAY-2000.

FT 29-OCT-1999; 99WO-US025495.

FT 30-OCT-1998; 98US-0106275P.

FT (MILLER) MILLER J L.

FT Miller JL;

FT WPI; 2000-365744/31.

FT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

FT Ib alpha molecule useful for producing antibodies which inhibit platelet

FT aggregation.

FT Claim 10; Page; 89pp; English.

FT The present sequence is that of the heavy chain variable region (VH) of

FT human single chain antibody (scFv) H1b-1 (see AA95198), which is

FT directed against platelet glycoprotein Ib (GPIb). The H1b series of scFv

CC

CC was isolated from a human synthetic VH and VL scFv library by 3 rounds of
 CC phagemid selection against transfectected CHO cells expressing the GPIb
 CC alpha component of the GPIb/IX/V complex on their surface, followed by a
 CC 4th round of selection against washed human platelets, and 2 final rounds
 CC in which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AA95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by Escherichia coli, the H1b scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences and
 CC are therefore attractive potential reagents for therapeutic purposes.
 CC They provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries, bypass
 CC grafts, dialysis etc., and can also be used as diagnostic reagents.
 CC Methods of inhibiting aggregation of platelets, of binding human platelet
 CC GPIIb/IIIa and of selecting a VH or VL region of an antibody that
 CC inhibits platelet aggregation are claimed. Note: The present sequence is
 CC not shown in the specification but is derived from the H1b-1 VH sequence
 CC given on page 71 (see AA95177)

SQ Sequence 113 AA;

Query Match 100.0%; Score 96; DB 3; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 17

DB 50 GINWNGSGTGYADSVK 66

RESULT 17

AA95189

ID AA95189 standard; protein; 115 AA.

XX AC AA95189;

XX DT 29-AUG-2000 (first entry)

XX DE Anti-platelet glycoprotein Ib human H1b-1 VH.

XX KW Variable heavy chain; single chain antibody; scFv; human; H1b-1;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 1..30 /note= "framework region 1"

FT Region 31..34 /note= "complementarity determining region 1"

FT Region 35..49 /note= "framework region 2"

FT Region 50..66 /note= "complementarity determining region 2"

FT Region 67..98 /note= "framework region 3"

FT Region 99..104 /note= "complementarity determining region 3"

FT Region 105..115 /note= "framework region 4"

FT WO200026667-A1.

FT 11-MAY-2000.

FT 29-OCT-1999; 99WO-US025495.

FT 30-OCT-1998; 98US-0106275P.

FT (MILLER) MILLER J L.

FT Miller J L.

FT WPI; 2000-365744/31.

FT Isolated nucleic acid molecule encoding anti-human platelet glycoprotein

FT Ib alpha molecule useful for producing antibodies which inhibit platelet

FT aggregation.

FT Claim 10; Page; 89pp; English.

FT The present sequence is that of the heavy chain variable region (VH) of

FT human single chain antibody (scFv) H1b-1 (see AA95198), which is

FT directed against platelet glycoprotein Ib (GPIb). The H1b series of scFv

CC

XX	24-NOV-1994.
PD	
XX	
XX	10-MAY-1993; 93WO-JP000603.
PF	
XX	
XX	10-MAY-1993; 93WO-JP000603.
PR	
XX	(NISB) JAPAN TOBACCO INC.
XX	
PA	Honjo T, Matsuda F;
XX	
PI	WPI; 1995-006791/01.
XX	N-PSDB; AAQ78958.
DR	
XX	DNA fragment comprising human immunoglobulin Vh genes - for the
PT	production of human immunoglobulin in mammalian hosts.
PT	
XX	Claim 29; Page 56-57; 130pp; Japanese.
PS	
XX	Protein sequences (AARG6295-51) are novel human immunoglobulin heavy
CC	chain sequences encoded by novel isolated genes. The genes (AAQ78939-
CC	79002) were isolated and cloned from a series of cosmid constructs: Y202;
CC	Y103; Y21; Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using
CC	primers AAQ78917-38. The genes are subdivided into 5 families of Vh
CC	genes. The fragments cover a region of 800 kb. The DNA fragments were
CC	isolated from high molecular weight DNA from human placenta. The DNA was
CC	partially digested with Taqi restriction enzyme. The fragments were
CC	separated by gel electrophoresis and 35-45 kb fractions were collected.
CC	The fragments were ligated with ClaI-digested cosmid vector pJB81. The
CC	ligation products were in vitro packed and infected into E.coli 490A. The
CC	fragments were then subcloned by colony hybridisation. The Vh genes and
CC	the DNA fragments encoding them are useful in producing human
CC	immunoglobulin in mammalian hosts. (Updated on 25-MAR-2003 to correct PN
CC	field.)
XX	
SQ	Sequence 117 AA;
	Query Match 100.0%; Score 96; DB 2; Length 117;
	Best Local Similarity 100.0%; Pred. No. 1.1e-06;
	Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 GINWNGGSGTYADSVKG 17
Db	69 GINWNGGSGTYADSVKG 85
	RESULT 21
ADXL01783	
ID	ADX01783 standard; protein; 117 AA.
XX	
AC	ADX01783;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	SARS coronavirus antibody heavy chain SEQ ID NO 39.
KW	severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
KW	respiratory disease; infection; antibody; heavy chain.
XX	
OS	SARS coronavirus.
XX	
FN	WO2005012360-A2.
XX	
PD	10-FEB-2005.
FF	21-JUL-2004; 2004WO-EP051568.
XX	
PR	22-JUL-2003; 2003WO-EP050328.
PR	01-SEP-2003; 2003WO-EP050391.
PR	16-OCT-2003; 2003WO-EP050723.
PR	24-NOV-2003; 2003WO-EP050883.
PR	04-DEC-2003; 2003WO-EP050943.
PR	02-FEB-2004; 2004WO-EP050067.

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PR 13-FEB-2004; 2004WO-EP050127.
PR 19-MAR-2004; 2004WO-EP050334.
PR 07-APR-2004; 2004WO-EP050464.
PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050543.
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
XX WPI; 2005-142879/15.
XX N-PSDB; ADX01782.
XX
XX New binding molecules that specifically bind to severe acute respiratory
XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
XX treating conditions resulting from SARS-CoV.
XX
XX Claim 4; SEQ ID NO 39; 633pp; English.
XX
XX The invention relates to a binding molecule, or its variant, capable of
XX specifically binding to a severe acute respiratory syndrome (SARS)-
XX coronavirus (CoV). The composition (including the binding molecule or its
XX functional variant, or the immunocjugate) is useful as a medicament for
XX the diagnosis, prophylaxis or treatment of a condition resulting from a
XX SARS-CoV, or in the preparation of the medicament. The present sequence
XX represents a SARS coronavirus binding molecule heavy chain.
XX
XX Sequence 117 AA;
XX
XX Query Match 100.0%; Score 96; DB 9; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GINWNGSGTGADSVK 17
XX |||||
XX Db 52 GINWNGSGTGADSVK 68
XX
XX RESULT 22
XX AAU02560
XX ID AAU02560 standard; protein; 118 AA.
XX AC AAU02560;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody heavy chain, FAT 46.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX N-ESDB; AAS03460.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 130; 182pp; English.
XX
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX SQ Sequence 118 AA;
XX
XX Query Match 100.0%; Score 96; DB 4; Length 118;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GINWNGSGTGADSVK 17
XX |||||
XX Db 50 GINWNGSGTGADSVK 66
XX
XX RESULT 23
XX AAU02605
XX ID AAU02605 standard; protein; 122 AA.
XX AC AAU02605;
XX
XX 05-DEC-2000 (first entry)
XX
XX Human anti-DAF antibody LU20 heavy chain variable region.
XX
XX LU20; human; antibody; VH domain; decay accelerating factor; DAF;
XX phage display; subtractive panning; lung cancer; lung carcinoma;
XX lung adenocarcinoma; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 26..32
XX /note= "hypervariable loop region"
XX Region 31..35
XX /label= CDR1
XX /note= "complementarity determining region I"
XX Region 50..56
XX /label= CDR2
XX /note= "complementarity determining region II"
XX Region 53..56
XX /note= "hypervariable loop residues"
XX Region 99..111
XX /label= CDR3
XX /note= "complementarity determining region III"
XX Region 100..110
XX /note= "hypervariable loop residues"
XX
XX WO200052054-A2.
XX
XX 08-SEP-2000.
XX
XX 29-FEB-2000; 2000WO-US005352.
XX
XX 01-MAR-1999; 99US-0122262P.
XX
XX (GETH ) GENENTECH INC.
XX

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PI Carter PJ, Ridgway JB;
 XX WPI; 2000-594169/56.
 XX Making antibodies (e.g. anti-decay accelerating factor antibody) for
 XX diagnosing or treating e.g. lung cancer comprises identifying an antigen
 XX that is differentially expressed on the surface of two or more distinct
 XX cell populations.
 XX Disclosure; Fig 5B; 52pp; English.
 XX The present sequence is that of the heavy chain variable region (VH) of
 XX the anti-decay accelerating factor (DAF) human antibody LU20. The VL
 XX region is given in AY06062. LU20 was produced using a novel method for
 XX making antibodies which can be used for cancer diagnosis or therapy. The
 XX method comprises: (a) binding an antibody phage from a naive antibody
 XX phage library to a live cancer cell; (b) selecting an antibody phage or
 XX antibody which binds selectively to the live cancer cell; and (c)
 XX identifying an antigen to which the antibody phage or antibody binds. To
 XX obtain LU20, a human scFv library was used to search for tumour-
 XX associated antigens by panning the lung adenocarcinoma cell line 1264,
 XX and counter-selecting with a non-tumour bronchial epithelial cell line,
 XX BEAS-2B. The invention also describes a method for identifying an antigen
 XX which is differentially expressed on the surface of 2 or more distinct
 XX cell populations. The anti-DAF human antibody, or a composition
 XX comprising the antibody, is useful for in vivo cancer diagnosis or
 XX therapy. In particular, the antibody is useful for diagnosing or treating
 XX lung cancer, e.g. small-cell lung cancer, non-small cell lung cancer,
 XX large cell lung carcinoma, lung adenocarcinoma, or squamous cell lung
 XX carcinoma (all claimed)
 XX SQ Sequence 122 AA;

Query Match 100.0%; Score 96; DB 3; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
 DB 50 GINWNGSGTGADSVK 66

RESULT 24
 ADJ57861
 ID ADJ57861 standard; protein; 123 AA.

XX AC ADJ57861;

XX DT 06-MAY-2004 (first entry)

XX DE Light variable clone of B28.

XX KW Cytostatic; Immunosuppressive; Antibacterial; Virucide; Fungicide;
 XX Antiparasitic; auto-immune disease; cancer; neoplastic disorder;
 XX leukemia.

XX OS Synthetic.

XX PN WO2004009618-A2.

XX PD 29-JAN-2004.

XX PF 15-JUL-2003; 2003WO-EP007690.

XX PR 18-JUL-2002; 2002EP-00077953.

XX PR 18-JUL-2002; 2002US-0397066P.

XX PR 27-MAY-2003; 2003WO-EP050201.

XX PA (CRUC-) CRUCCELL HOLLAND BV.

XX PI Van Berkel PHC, Brus RHP, Bout A, Logtenberg T;

XX WPI; 2004-132914/13.

DR N-PSDB; ADJ57860.

XX Producing mixture of antibodies in recombinant host comprises expressing
 XX nucleic acid sequence(s) encoding light chain and three different heavy
 XX chains capable of pairing with light chain in recombinant host cell.
 XX Disclosure; SEQ ID NO 12; 186pp; English.

XX The present invention relates to producing a mixture of antibodies in a
 XX recombinant host comprises expressing in a recombinant host cell a
 XX nucleic acid sequence or nucleic acid sequences encoding a light chain
 XX and at least three different heavy chains that are capable of pairing
 XX with a light chain. The method is useful for producing a mixture of a
 XX antibodies in a recombinant host, is useful for the preparation of a
 XX medicament for use in the treatment or diagnosis of a disease or disorder
 XX in a human or animal. The antibodies are useful for treating auto-immune
 XX disease and cancer such as solid tumors of the brain, head and neck,
 XX breast, prostate, colon, lung, etc., hematologic tumors such as B-cell
 XX tumors, neoplastic disorders such as leukemia, lymphoma, sarcoma,
 XX carcinoma, neural cell tumors, myelomas, melanomas, neuroblastomas, etc,
 XX and are also useful for treating graft-versus-host rejections, infectious
 XX diseases due to pathogenic bacteria such as multidrug resistant
 XX Staphylococcus aureus, fungi such as Candida albicans, as prophylaxis
 XX against viruses such as rabies virus, for treating or preventing disease
 XX caused by adenoviruses, respiratory syncytium virus, and for treating
 XX diseases caused by unicellular or multicellular parasites. The method
 XX enables exploring many combinations simultaneously, where the
 XX combinations include the presence of bispecific antibodies in the
 XX produced mixture. The present sequence represents the light variable
 XX clone of B28.

XX SQ Sequence 123 AA;

Query Match 100.0%; Score 96; DB 8; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
 DB 52 GINWNGSGTGADSVK 68

RESULT 25

AAU98019

ID AAU98019 standard; protein; 207 AA.

XX AC AAU98019;

XX DT 27-AUG-2002 (first entry)

XX DE Human acetylcholinesterase antibody PD-antihASP 3.

XX KW Human; synaptic acetylcholinesterase; PD-antihASP 3; antibody;
 XX single-chain variable fragment; scFv; AChE-S;
 XX heavy chain variable region; progressive neuromuscular disorder;
 XX muscle distortion; muscle re-innervation; myasthenia gravis;
 XX neuromuscular junction abnormality; Eaton-Lambert disease;
 XX muscular dystrophy; amyotrophic lateral sclerosis; ALS;
 XX post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
 XX post-stroke sclerosis; post-injury muscle damage;
 XX excessive re-innervation.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 201

XX FT /label= Unknown
 XX FT /note= "Encoded by GNA"

XX PN WO200246422-A1.

XX PD 13-JUN-2002.

PF 22-MAY-2001; 2001WO-IL000464.
 XX 04-DEC-2000; 2000IL-00140071.
 PR (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX Soreq H, Flores CF, Nissim A;
 XX WPI; 2002-463832/49.
 DR N-PSDB; ABK52917.
 XX Nucleic acid sequence coding for a single-chain variable fragment (scFv)
 PT antibody that has specific affinity for the synaptic variant of
 PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
 PT disorder, e.g. Myasthenia gravis.
 XX
 XX Claim 11; Page 65-66; 73pp; English.
 XX The invention relates to a nucleic acid sequence coding for a single-
 CC chain variable fragment (scFv) antibody that has specific affinity for
 CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
 CC antibody consists essentially of a polypeptide comprising the binding
 CC portion of the heavy chain variable region of an antibody. Also included
 CC are an expression vehicle comprising a nucleic acid sequence coding for a
 CC scFv antibody that has specific affinity for the synaptic variant of AChE
 CC -S, an scFv antibody specifically recognising and binding to the synaptic
 CC variant of AChE-S and a method for the diagnosis of a progressive
 CC neuromuscular disorder in a mammal, comprising obtaining a sample from
 CC the mammal and detecting intensified expression of at least one of the
 CC AChE variants in the sample. The single-chain Fv antibody is useful for
 CC diagnosing a progressive neuromuscular disorder which involves any one of
 CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
 CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
 CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
 CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dysconia, post
 CC -stroke sclerosis, post-injury muscle damage, excessive re-innervation,
 CC or post-exposure to AChE inhibitors. The present sequence represents an
 CC anti-AChE scFv antibody, PD-antibASP 3
 XX
 XX Sequence 207 AA;
 SQ
 Query Match 100.0%; Score 96; DB 5; Length 207;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GINWNGGSTGYADSVKG 17
 Db 72 GINWNGGSTGYADSVKG 88
 RESULT 26
 ADR28086
 ID ADR28086 standard; protein; 235 AA.
 XX
 AC ADR28086;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE NPB polypeptide scFv31, seq id 33.
 XX
 XX Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.
 XX
 XX Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 88. .94
 FT Region /note= "complementary determining region claimed under
 FT claim 5"
 XX
 XX WO2004056874-A2.
 PN
 , XX

PD 08-JUL-2004.
 XX 22-DEC-2003; 2003WO-EP014756.
 XX 20-DEC-2002; 2002US-0435893P.
 PR 15-JAN-2003; 2003EP-00000615.
 XX (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.
 XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Niewoehner J;
 PI Jay DG, Eustace BK, Knauer R, Jensen KH;
 XX WPI; 2004-507700/48.
 DR N-PSDB; ADR28120.
 XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
 PT that modulates neuropilin-1 function or inhibits NP-1 dependent
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 PT for treating cancer.
 XX Claim 3; SEQ ID NO 33; 120pp; English.
 XX The invention relates to a neuropilin binder (NPB) (I) which is a
 CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
 CC disclosed is an ex vivo method of determining the dependency of the
 CC invasiveness of a naturally occurring invasive cancer cell on the
 CC functionality of NP-1. The NPB of the invention is an inhibitor of
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
 CC is useful for detecting NP-1 expression, modulation of NP-1 function, or
 CC particularly modulation or inhibition of NP-dependent invasion or
 CC adhesion of cells, preferably tumour cells. It is useful in the
 CC manufacture of medicament for the treatment or prevention of NP-dependent
 CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 96; DB 8; Length 235;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GINWNGGSTGYADSVKG 17
 Db 39 GINWNGGSTGYADSVKG 55
 RESULT 27
 AAY95198
 ID AAY95198 standard; protein; 238 AA.
 XX
 AC AAY95198;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Anti-platelet glycoprotein Ib human scFv H1b-1.
 XX
 KW Single chain antibody; scFv; human; H1b-1; glycoprotein Ib alpha;
 KW platelet; aggregation; antiaggregant; antithrombotic; thrombus; therapy;
 KW diagnostic.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Region 1. .113

FT Region /note= "heavy chain variable region"
FT 1..30
FT /note= "framework region 1"
FT 31..34
FT /note= "complementarity determining region 1"
FT 35..49
FT /note= "framework region 2"
FT 50..66
FT /note= "complementarity determining region 2"
FT 67..98
FT /note= "framework region 3"
FT 99..104
FT /note= "complementarity determining region 3"
FT 105..113
FT /note= "framework region 4"
FT 114..130
FT /note= "vector-derived linker"
FT 131..238
FT Region /note= "light chain variable region"
FT 131..152
FT /note= "framework region 1"
FT 153..163
FT /note= "complementarity determining region 1"
FT 164..178
FT /note= "framework region 2"
FT 179..185
FT /note= "complementarity determining region 2"
FT 186..217
FT /note= "framework region 3"
FT 218..226
FT /note= "complementarity determining region 3"
FT 227..238
FT /note= "framework region 4"
FT
FT
XX WO200026667-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025495.
XX
XX 30-OCT-1998; 98US-0106275P.
XX
XX (MILLER) MILLER J L.
XX
XX Miller JL;
XX
XX WPI; 2000-365744/31.
XX
XX Isolated nucleic acid molecule encoding anti-human platelet glycoprotein
XX Ib alpha molecule useful for producing antibodies which inhibit platelet
XX aggregation.
XX
XX Disclosure; Fig 5; 89pp; English.
XX
XX The present sequence is that of human single chain antibody (scFv) H1b-1,
XX which is directed against platelet glycoprotein Ib (GPIb). H1b-1 is
XX composed of a heavy chain variable region (see AA95189) and light chain
XX variable region (see AA95194) joined via a peptide linker. The H1b
XX scFv was isolated from a human synthetic VH and VL scFv library
XX by 3 rounds of phagemid selection against transfected CHO cells
XX expressing the GPIb alpha component of the GPIb/IX/V complex on their
XX surface, followed by a 4th round of selection against washed human
XX platelets, and 2 final rounds in which attempts were made to displace
XX scFv from washed platelets by flooding with murine monoclonal antibody or
XX mimotope peptide (see AA95229). Whether displayed as surface proteins on
XX a phagemid or secreted as free scFv by Escherichia coli, the H1b scFv
XX clones are capable of inhibiting von Willebrand factor-dependent
XX aggregation of platelets. The scFv are composed of native human protein
XX sequences and are therefore attractive potential reagents for therapeutic
XX purposes. They provide a new class of antithrombotic agents, useful for
XX the prevention of platelet-dependent thrombi in diseased arteries, bypass
XX grafts, dialysis etc., and can also be used as diagnostic reagents.
XX Methods of inhibiting aggregation of platelets, of binding human platelet

CC GPIb alpha and of selecting a VH or VL region of an antibody that
CC inhibits platelet aggregation are claimed
XX
XX Sequence 238 AA;
SQ
Query Match 100.0%; Score 96; DB 3; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGYADSVKG 17
DB 50 GINWNGSGTGYADSVKG 66
RESULT 28
ABP46004
ID ABP46004 standard; protein; 239 AA.
XX
XX AC ABP46004;
DT 19-AUG-2002 (first entry)
XX
XX Human BlyS binding scFv SEQ ID 2015.
DE
XX
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240818P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2804-2805; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of

```
CC the invention
XX
SQ Sequence 239 AA;
    Query Match      100.0%; Score 96; DB 5; Length 239;
    Best Local Similarity 100.0%; Pred. No. 2.5e-06;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GINWNGGSTGYADSVK 17
    |||||
Db 50 GINWNGGSTGYADSVK 66

RESULT 29
ABP46027
ID ABP46027 standard; protein; 239 AA.
XX
AC ABP46027;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 2038.
XX
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulator; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
(PUMA-) HUMAN GENOME SCI INC.
(PAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
WPI; 2002-114799/15.
XX
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
diagnosis and treatment of cancers and immune disorders.
XX
Claim 1; Page 2830-2831; 3148pp; English.
XX
This invention describes novel antibodies that immunospecifically bind to
B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
antirheumatic and antiAIDS activity and can be used in vaccines to
inhibit the expression and activity of BlyS. The antibodies bind to BlyS
and so may be used to detect and quantitate the presence of BlyS in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of BlyS. They may also be
administered to treat diseases associated with aberrant BlyS expression
and activity such as cancer, immune, and autoimmune disorders and
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method of
the invention
XX
```

```
CC the invention
XX
SQ Sequence 239 AA;
    Query Match      100.0%; Score 96; DB 5; Length 239;
    Best Local Similarity 100.0%; Pred. No. 2.5e-06;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GINWNGGSTGYADSVK 17
    |||||
Db 50 GINWNGGSTGYADSVK 66

RESULT 30
ABP44926
ID ABP44926 standard; protein; 239 AA.
XX
AC ABP44926;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 937.
XX
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulator; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
(HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
WPI; 2002-114799/15.
XX
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
diagnosis and treatment of cancers and immune disorders.
XX
Claim 1; Page 1520-1521; 3148pp; English.
XX
This invention describes novel antibodies that immunospecifically bind to
B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
tumour necrosis factor (TNF) super family and induces B cell
proliferation and differentiation. The antibodies of the invention have
cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
antirheumatic and antiAIDS activity and can be used in vaccines to
inhibit the expression and activity of BlyS. The antibodies bind to BlyS
and so may be used to detect and quantitate the presence of BlyS in
biological samples and may be used in this way to diagnose disease
associated with aberrant expression of BlyS. They may also be
administered to treat diseases associated with aberrant BlyS expression
and activity such as cancer, immune, and autoimmune disorders and
diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method of
the invention
XX
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SQ      Sequence 239 AA;
Query Match      100.0%; Score 96; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
        |||||
Db       50 GINWNGSGTGYADSVKG 66

RESULT 31
ADG95753
ID      ADG95753 standard; protein; 239 AA.
XX
AC      ADG95753;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Single chain antibody that immunospecifically binds BlyS SeqID 937.
XX
KW      antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW      B cell proliferation; differentiation; scFv; myasthenia gravis;
KW      multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW      carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW      antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS      Unidentified.
XX
PN      WO2003055979-A2.
XX
PD      10-JUL-2003.
XX
PF      14-NOV-2002; 2002WO-US036496.
XX
PR      16-NOV-2001; 2001US-0331469P.
PR      19-DEC-2001; 2001US-0340817P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
WPI; 2003-505530/47.
XX
Novel antibody that immunospecifically binds to a B lymphocyte stimulator
(BlyS), useful for detecting and treating diseases or disorders e.g.
rheumatoid arthritis, asthma and leukemia.
XX
Example 1; SEQ ID NO 937; 394pp; English.
XX
This invention relates to novel antibodies that immunospecifically bind
to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
chromosome 13q34 and encodes a protein that is a member of the tumour
necrosis factor superfamily and induces both in vivo and in vitro B cell
proliferation and differentiation. Specifically, it refers to single
chain antibody molecules (scFvs) derived, preferably, from the variable
heavy CD3 region that immunospecifically bind to a polypeptide, or
fragment thereof, of either human, murine, rat or monkey BlyS. The
present invention refers to the use of such antibodies in various methods
for the detection, diagnosis and prognosis of diseases related to the
aberrant expression or inappropriate function of BlyS or its receptor. As
such, these compositions are useful for identifying immune disorders
including myasthenia gravis and multiple sclerosis, inflammatory
disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
as AIDS and proliferative disorders including leukaemia, carcinoma and
lymphoma. Accordingly, they can be described as exhibiting various
activities such as antirheumatic, antiarthritic, neuroprotective,
antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
polypeptide sequence is a single chain antibody that binds BlyS of the
invention. NOTE: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
XX
SQ      Sequence 239 AA;
Query Match      100.0%; Score 96; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GINWNGSGTGYADSVKG 17
        |||||
Db       50 GINWNGSGTGYADSVKG 66

RESULT 32
ADG96854
ID      ADG96854 standard; protein; 239 AA.
XX
AC      ADG96854;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Single chain antibody that immunospecifically binds BlyS SeqID 2038.
XX
KW      antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW      B cell proliferation; differentiation; scFv; myasthenia gravis;
KW      multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW      carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW      antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS      Unidentified.
XX
PN      WO2003055979-A2.
XX
PD      10-JUL-2003.
XX
PF      14-NOV-2002; 2002WO-US036496.
XX
PR      16-NOV-2001; 2001US-0331469P.
PR      19-DEC-2001; 2001US-0340817P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
WPI; 2003-505530/47.
XX
Novel antibody that immunospecifically binds to a B lymphocyte stimulator
(BlyS), useful for detecting and treating diseases or disorders e.g.
rheumatoid arthritis, asthma and leukemia.
XX
Example 1; SEQ ID NO 2038; 394pp; English.
XX
This invention relates to novel antibodies that immunospecifically bind
to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
chromosome 13q34 and encodes a protein that is a member of the tumour
necrosis factor superfamily and induces both in vivo and in vitro B cell
proliferation and differentiation. Specifically, it refers to single
chain antibody molecules (scFvs) derived, preferably, from the variable
heavy CD3 region that immunospecifically bind to a polypeptide, or
fragment thereof, of either human, murine, rat or monkey BlyS. The
present invention refers to the use of such antibodies in various methods
for the detection, diagnosis and prognosis of diseases related to the
aberrant expression or inappropriate function of BlyS or its receptor. As
such, these compositions are useful for identifying immune disorders
including myasthenia gravis and multiple sclerosis, inflammatory
disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
as AIDS and proliferative disorders including leukaemia, carcinoma and
lymphoma. Accordingly, they can be described as exhibiting various
activities such as antirheumatic, antiarthritic, neuroprotective,
antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
polypeptide sequence is a single chain antibody that binds BlyS of the
invention. NOTE: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
XX
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SQ Sequence 239 AA;
Query Match      100.0%; Score 96; DB 7; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
   |||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 33
ADG96831
ID ADG96831 standard; protein; 239 AA.
XX
AC ADG96831;
XX
DT 11-MAR-2004 (first entry)
DE
DE Single chain antibody that immunospecifically binds Blys SeqID 2015.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
XX antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Baraeh SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 2015; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antirheumatic, antiarthritic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX

SQ Sequence 239 AA;
Query Match      100.0%; Score 96; DB 7; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
   |||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 34
ADG30497
ID ADG30497 standard; protein; 242 AA.
XX
AC ADG30497;
XX
DT 26-FEB-2004 (first entry)
DE
DE Human GMCC127 scFv protein.
XX
XX GMAD; VH; CDR; complementarity determining region; VL; scFv;
XX single chain antibody; antidiabetic; type II diabetes; human; GMCC127.
XX
XX Homo sapiens.
XX
XX WO2003085093-A2.
XX
XX 16-OCT-2003.
XX
XX 28-MAR-2003; 2003WO-US009625.
XX
XX 01-APR-2002; 2002US-0368813P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Baker KP, Albert VR, Chowdhury P;
XX
XX WPI; 2003-804305/75.
XX
XX N-PSDB; ADG30594.
XX
XX New antibody that specifically binds to GMAD polypeptide, useful for
XX diagnosing, monitoring, treating, preventing or ameliorating type II
XX diabetes.
XX
XX Claim 2; SEQ ID NO 130; 410pp; English.
XX
XX The invention relates to a novel antibody that specifically binds to a
XX GMAD polypeptide comprising a first amino acid sequence that is at least
XX 95% identical to a second amino acid sequence of a VH CDR
XX (complementarity determining region) or VL CDR of an scFv (single chain
XX antibody molecule). The antibody of the invention demonstrates
XX antidiabetic activity and may be useful for diagnosing, monitoring,
XX treating, preventing or ameliorating type II diabetes. The current
XX sequence is that of the human scFv protein of the invention.
XX
XX Sequence 242 AA;
Query Match      100.0%; Score 96; DB 7; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
   |||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 35
AD158068
ID AD158068 standard; protein; 242 AA.
XX
XX AD158068;
XX
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DT 22-APR-2004 (first entry)
XX Reg IV-specific single chain antibody fragment (scFv) #27.
DE antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;
XX inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
KW diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
KW cancer; human.
XX Homo sapiens.
OS WO2004003144-A2.
XX 08-JAN-2004.
XX 26-JUN-2003; 2003WO-US019908.
XX 01-JUL-2002; 2002US-0392382P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA;
PI WPI; 2004-071976/07.
XX N-PSDB; ADI58134.
XX Novel antibody, useful for treating, preventing or ameliorating
PT inflammatory bowel disorder, cancer of the gastrointestinal tract or
PT diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
XX Claim 2; SEQ ID NO 28; 324pp; English.
XX The invention comprises an antibody that specifically binds a
CC regeneration IV (Reg IV) protein. The invention specifically comprises
CC the amino acid and coding sequences of single chain antibody fragments
CC (scFv's) that bind Reg IV protein. The antibody of the invention is
CC useful for treating, preventing and ameliorating: inflammatory bowel
CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.
CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer
CC of the gastrointestinal tract. The antibody of the invention is also
CC useful for detecting the expression of a Reg IV protein. The present
CC amino acid sequence represents an scFv of the invention.
XX
SQ Sequence 242 AA;
Query Match 100.0%; Score 96; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGADSVKVG 17
DB 50 GINWNGSGTGADSVKVG 66
RESULT 36
AAO31136
ID AAO31136 standard; protein; 244 AA.
XX AAO31136;
XX 06-OCT-2003 (first entry)
DT Human CM005G08 scFv protein that specifically binds TR7.
XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW complementarity determining region; CDR; light chain variable domain; VL;
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW glioblastoma; graft versus host disease; antibody therapy; neurotropic;
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW immunosuppressive; neuroprotective; antibody therapy; antibody.
XX

OS Homo sapiens.
XX WO2003054216-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US040597.
XX 20-DEC-2001; 2001US-0341237P.
XX 05-APR-2002; 2002US-0369877P.
XX 04-JUN-2002; 2002US-0384828P.
XX 18-JUL-2002; 2002US-0396591P.
XX 15-AUG-2002; 2002US-0403370P.
XX 13-NOV-2002; 2002US-0425737P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
PI WPI; 2003-569250/53.
XX N-PSDB; AAL62833.
XX New antibody or its fragment, useful for treating, preventing or
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
PT disease, AIDS.
XX Claim 2; Page 277-278; 301pp; English.
XX The invention relates to an isolated antibody or its fragments such as
CC VHCDR1 (heavy chain variable domain complementarity determining region),
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC antibody or its fragment is useful for treating, preventing or
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC a neurodegenerative disorder. The invention is useful in antibody
CC therapy. The present sequence is human scFv protein that specifically
CC binds TR7
XX
SQ Sequence 244 AA;
Query Match 100.0%; Score 96; DB 6; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GINWNGSGTGADSVKVG 17
DB 50 GINWNGSGTGADSVKVG 66
RESULT 37
ADW90315
ID ADW90315 standard; protein; 244 AA.
XX ADW90315;
XX ADW90315;
XX 21-APR-2005 (first entry)
DT Phage scFv SARS antibody SEQ ID NO 585.
XX Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
KW respiratory-gen.; infection; respiratory disease; antibody.
XX SARS coronavirus.
OS WO2005012337-A2.
XX

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PD 10-FEB-2005.
XX
PF 15-JUL-2004; 2004WO-EP051498.
XX
XX 15-JUL-2003; 2003WO-EP050308.
PR 24-JUL-2003; 2003WO-EP050333.
PR 02-SEP-2003; 2003WO-EP050392.
PR 27-OCT-2003; 2003WO-EP050761.
PR 24-NOV-2003; 2003WO-EP050883.
XX
PA (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, Goudsmit J, Slootstra JW, Timmerman P, De Kruif CA;
PI Van Den Brink EN;
XX
XX WPI; 2005-162947/17.
DR
XX
XX New antigenic peptides from severe acute respiratory syndrome-coronavirus
PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
PT preventing SARS-CoV infection.
XX
PS Example 2; SEQ ID NO 585; 199pp; English.
XX
CC The invention relates to an antigenic peptide from severe acute
CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
CC molecule encoding the peptide, fusion protein, conjugate or antibody is
CC useful in preparing a composition for diagnosing, treating or preventing
CC SARS-CoV infection. The present sequence represents a phage scFv SARS
CC antibody.
XX
SQ Sequence 244 AA;
Query Match 100.0%; Score 96; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSGTYADSVKG 17
Db |||||
53 GINWNGGSGTYADSVKG 69

RESULT 38
ADX01815
ID ADX01815 standard; protein; 244 AA.
XX
AC ADX01815;
XX
DT 21-APR-2005 (first entry)
XX
XX SARS coronavirus scFv antibody SEQ ID NO 71.
XX
XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX respiratory disease; infection; antibody.
XX
OS SARS coronavirus.
XX
XX WO2005012360-A2.
XX
XX 10-FEB-2005.
XX
XX 21-JUL-2004; 2004WO-EP051568.
XX
XX 22-JUL-2003; 2003WO-EP050328.
PR 01-SEP-2003; 2003WO-EP050391.
PR 16-OCT-2003; 2003WO-EP050723.
PR 24-NOV-2003; 2003WO-EP050883.
PR 04-DEC-2003; 2003WO-EP050943.
PR 02-FEB-2004; 2004WO-EP050067.
PR 13-FEB-2004; 2004WO-EP050127.
PR 19-MAR-2004; 2004WO-EP050334.
PR 07-APR-2004; 2004WO-EP050464.
PR 14-APR-2004; 2004WO-EP050516.
PR 29-APR-2004; 2004WO-EP050643.

XX
XX (CRUC-) CRUCELL HOLLAND BV.
XX
XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;
PI N-PSDS; ADX01814.
XX
XX WPI; 2005-142879/15.
DR
XX
XX New binding molecules that specifically bind to severe acute respiratory
PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
PT treating conditions resulting from SARS-CoV.
XX
XX Example 3; SEQ ID NO 71; 633pp; English.
XX
XX The invention relates to a binding molecule, or its variant, capable of
XX specifically binding to a severe acute respiratory syndrome (SARS)-
XX coronavirus (CoV). The composition (including the binding molecule or its
XX functional variant, or the immunoconjugate) is useful as a medicament for
XX the diagnosis, prophylaxis or treatment of a condition resulting from a
XX SARS-CoV, or in the preparation of the medicament. The present sequence
XX represents a SARS coronavirus scFv.
XX
SQ Sequence 244 AA;
Query Match 100.0%; Score 96; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSGTYADSVKG 17
Db |||||
53 GINWNGGSGTYADSVKG 69

RESULT 39
ADY34209
ID ADY34209 standard; protein; 244 AA.
XX
AC ADY34209;
XX
DT 05-MAY-2005 (first entry)
XX
XX TRAIL receptor TR7 scFv CM005G08.
XX
XX TRAIL receptor; antibody therapy; cytostatic; immunosuppressive;
XX anti-HIV; neuroprotective; gene therapy; cancer; neoplasm; colon tumor;
XX breast tumor; uterine cervix tumor; pancreas tumor; lung tumor;
XX gastrointestinal tumor; Kaposi's sarcoma; central nervous system tumor;
XX graft versus host disease; acquired immune deficiency syndrome;
XX neurodegenerative disease; diagnosis; single chain antibody.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Domain 1. .121
FT /label = VH
FT /note = "Heavy chain variable region domain"
FT 26. .35
FT /label = CDR1
FT /note = "Complementarity determining region 1"
FT 50. .66
FT /label = CDR2
FT /note = "Complementarity determining region 2"
FT 99. .110
FT /label = CDR3
FT /note = "Complementarity determining region 3"
FT 136. .244
FT /label = VL
FT /note = "Light chain variable region domain"
FT 158. .168
FT /label = CDR1
FT /note = "Complementarity determining region 1"
FT 184. .190
FT /label = CDR2

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FT Region /note= "Complementarity determining region 2"
FT 223.. 233
FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO2005016236-A2.
XX 24-FEB-2005.
XX 05-MAY-2004; 2004WO-US013900.
XX 06-MAY-2003; 2003US-0468092P.
XX 15-AUG-2003; 2003US-0495140P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Salcedo T, Rosen CA, Albert VR, Humphreys R, Vaughan TJ;
XX WPI; 2005-173213/18.
XX N-PSDB; ADY34224.
XX New antibodies that immunospecifically bind to tumor necrosis factor-
XX related apoptosis-inducing ligand (TRAIL) receptor TR7, useful for
XX diagnosing, preventing or treating e.g. cancer, AIDS or neurodegenerative
XX disorders.
XX Claim 1; SEQ ID NO 42; 342pp; English.
XX The present sequence is the protein sequence of CM005G08, a single chain
XX antibody (scFv) that immunospecifically binds to the TRAIL receptor, TR7
XX ADY34170. The invention relates to antibodies that preferentially bind to
XX TR7 relative to their ability to bind to TR1, TR5, TR4 or TR10. Phase
XX display technology was used to identify scFvs ADY34209-ADY34223,
XX including the present scFv, that immunospecifically bind to TR7.
XX Molecules comprising or consisting of fragments or variants of these
XX scFvs (including heavy chain variable domains and their CDRs and light
XX chain variable domains and their CDRs) that immunospecifically bind to
XX TR7 or its fragments or variants are also encompassed by the invention,
XX as are the nucleic acid molecules ADY34224-ADY34238 that encode these
XX scFvs and/or molecules. An antibody of the invention may be a whole
XX immunoglobulin molecule, an scFv, a monoclonal antibody, human antibody,
XX chimeric antibody, humanized antibody, Fab fragment, Fab' fragment,
XX F(ab')2, Fv or disulfide linked Fv, and may be conjugated to a therapeutic
XX or cytotoxic agent. The antibody (or fragment) can be used in a claimed
XX method of treating, preventing or ameliorating a cancer in an animal,
XX including a human. The cancer is colon cancer, breast cancer, uterine
XX cancer, pancreatic cancer, lung cancer, gastrointestinal cancer, Kaposi's
XX sarcoma, or cancer of the central nervous system such as
XX medulloblastoma, neuroblastoma or glioblastoma. The antibody (or
XX fragment) can also be used to treat, prevent or ameliorate graft versus host
XX disease, AIDS or a neurodegenerative disorder. Methods are also provided
XX for: inhibiting the growth, or of killing, TR7 expressing cells using an
XX antibody of the invention; detecting the expression of a TR7 polypeptide
XX using the antibody; and detecting, diagnosing, prognosing or monitoring
XX cancers and other hyperproliferative disorders by comparing the level of
XX a TR7 polypeptide with a standard level of TR7 polypeptide.
XX Sequence 244 AA;
XX Query Match 100.0%; Score 96; DB 9; Length 244;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GINWNGSGTGADSVKVG 17
XX |||||
XX 50 GINWNGSGTGADSVKVG 66
XX
XX RESULT 40
XX ABG78329
XX ID ABG78329 standard; protein; 246 AA.
XX XX
XX AC ABG78329;
XX
XX 15-NOV-2002 (first entry)
XX Human Fv molecule hypervariable region related peptide #204.
XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX Homo sapiens.
XX WO200259264-A2.
XX 01-AUG-2002.
XX 31-DEC-2001; 2001WO-US049440.
XX 29-DEC-2000; 2000US-00751181.
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX Plaksin D, Peretz T;
XX WPI; 2002-619166/66.
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX or fragment, or construct of fragment with enhanced binding
XX characteristics so as to selectively bind target cell in favor of other
XX cells.
XX Disclosure; Page 44-45; 232pp; English.
XX The invention relates to a peptide or polypeptide comprising an Fv
XX molecule, a construct or fragments or a construct of a fragment with
XX enhanced binding characteristics which selectively and/or specifically
XX binds to a target cell in favour of other cells, where binding is
XX primarily determined by a first hypervariable region and Fv is a single
XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX association with or attached, coupled, combined, linked or fused to a
XX pharmaceutical agent, is useful in the manufacture of a medicament, where
XX the medicament has activity against a diseased cell, preferably a cancer
XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX composition for use in inhibiting the growth of a diseased or cancer
XX cell. This sequence represents a human Fv molecule hypervariable region
XX related peptide of the invention
XX Sequence 246 AA;
XX Query Match 100.0%; Score 96; DB 5; Length 246;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GINWNGSGTGADSVKVG 17
XX |||||
XX 51 GINWNGSGTGADSVKVG 67
XX
XX Search completed: November 18, 2005, 21:08:13
XX Job time : 219.357 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 18, 2005, 21:02:00 ; Search time 54.0357 Seconds
(without alignments)
26.010 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSGTGVADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*

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4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	98	2	US-10-194-975-20
2	96	100.0	98	2	US-09-534-717-599
3	96	100.0	116	1	US-08-652-816A-14
4	96	100.0	117	2	US-08-545-809A-106
5	96	100.0	117	2	US-09-515-697-106
6	96	100.0	309	2	US-09-079-029-9
7	79	82.3	17	2	US-09-424-840B-109
8	79	82.3	98	2	US-09-534-717-598
9	79	82.3	99	2	US-10-194-975-16
10	79	82.3	118	2	US-08-545-809A-97
11	79	82.3	118	2	US-09-515-697-97
12	79	82.3	119	2	US-09-840-459-88
13	79	82.3	119	2	US-09-497-625A-88
14	79	82.3	120	1	US-08-958-201-8
15	79	82.3	120	1	US-08-958-201-10
16	74	77.1	149	2	US-09-471-276-898
17	71	74.0	17	2	US-09-424-840B-114
18	71	74.0	98	2	US-09-534-717-600
19	71	74.0	98	2	US-09-534-717-612
20	71	74.0	98	2	US-09-534-717-614
21	71	74.0	98	2	US-08-896-535-75
22	71	74.0	99	2	US-10-194-975-27
23	71	74.0	117	2	US-08-545-809A-119
24	71	74.0	117	2	US-09-515-697-119
25	71	74.0	118	2	US-08-545-809A-125
26	71	74.0	118	2	US-09-515-697-125
27	71	74.0	124	2	US-09-424-840B-18
28	70.8	68	68	68	US-07-942-245-24
29	68	68.8	68	68	US-09-232-290-35
30	66	68.8	17	2	US-09-424-840B-70
31	66	68.8	17	2	US-09-424-840B-78
32	66	68.8	124	2	US-09-424-840B-123
33	63	65.6	126	2	US-08-983-607-26
34	62.5	65.1	117	2	US-09-157-370-1
35	62	64.6	17	1	US-08-264-093-22
36	62	64.6	89	2	US-09-840-459-48
37	62	64.6	89	2	US-09-497-625A-48
38	62	64.6	98	2	US-09-534-717-620
39	62	64.6	98	2	US-09-534-717-621
40	62	64.6	98	2	US-09-534-717-633
41	62	64.6	98	2	US-09-534-717-634
42	62	64.6	111	2	US-09-899-896-7
43	62	64.6	118	1	US-08-652-816A-11
44	62	64.6	120	1	US-08-264-093-14
45	62	64.6	268	2	US-09-976-118-1
46	62	64.6	483	2	US-09-043-672A-5
47	61.5	64.1	95	2	US-09-043-514-2
48	61.5	64.1	97	2	US-10-194-975-29
49	61.5	64.1	97	2	US-10-194-975-31
50	61.5	64.1	97	2	US-09-534-717-616
51	61.5	64.1	116	2	US-08-545-809A-135
52	61.5	64.1	116	2	US-09-515-697-135
53	61	63.5	98	2	US-10-194-975-22
54	61	63.5	98	2	US-09-534-717-613
55	61	63.5	98	2	US-09-534-717-619
56	61	63.5	98	2	US-08-896-535-74
57	61	63.5	113	2	US-08-974-899-6
58	61	63.5	113	2	US-09-795-798-6
59	61	63.5	113	2	US-08-908-469-11
60	61	63.5	116	2	US-09-184-688-48
61	61	63.5	116	2	US-08-983-607-36
62	61	63.5	116	2	US-09-504-262D-48
63	61	63.5	116	2	US-09-840-459-80
64	61	63.5	116	2	US-09-497-625A-80
65	61	63.5	117	2	US-08-545-809A-103
66	61	63.5	117	2	US-08-545-809A-109
67	61	63.5	117	2	US-08-983-607-46
68	61	63.5	117	2	US-09-840-459-83
69	61	63.5	117	2	US-09-497-625A-83
70	61	63.5	117	2	US-09-515-697-103
71	61	63.5	117	2	US-09-515-697-109
72	61	63.5	118	1	US-08-652-816A-12
73	61	63.5	119	2	US-09-648-067A-15
74	61	63.5	119	2	US-09-602-812A-6
75	61	63.5	120	1	US-08-428-197-20
76	61	63.5	120	1	US-08-428-197-22
77	61	63.5	120	1	US-08-428-197-24
78	61	63.5	120	1	US-08-428-197-26
79	61	63.5	120	1	US-08-428-197-28
80	61	63.5	120	1	US-08-428-197-30
81	61	63.5	120	1	US-08-428-197-32
82	61	63.5	120	1	US-08-428-197-34
83	61	63.5	120	1	US-08-428-197-40
84	61	63.5	120	2	US-09-025-769B-38
85	61	63.5	120	2	US-09-025-769B-38
86	61	63.5	120	2	US-09-490-070A-38
87	61	63.5	120	2	US-09-490-070A-63
88	61	63.5	120	2	US-09-840-459-85
89	61	63.5	120	2	US-09-490-153-38
90	61	63.5	120	2	US-09-490-153-63
91	61	63.5	120	2	US-09-497-625A-85
92	61	63.5	120	2	US-09-490-324-38
93	61	63.5	120	2	US-09-490-324-63
94	61	63.5	120	4	PCT-US93-07832-4
95	61	63.5	120	4	PCT-US93-10555-20
96	61	63.5	120	4	PCT-US93-10555-22
97	61	63.5	120	4	PCT-US93-10555-24
98	61	63.5	120	4	PCT-US93-10555-26
99	61	63.5	120	4	PCT-US93-10555-28
100	61	63.5	120	4	PCT-US93-10555-30

ALIGNMENTS

RESULT 1
US-10-194-975-20
; Sequence 20, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-20

Query Match 100.0%; Score 96; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 GINWGGSTGYADSVKG 66

RESULT 2
US-09-534-717-599
; Sequence 599, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-599

Query Match 100.0%; Score 96; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 GINWGGSTGYADSVKG 66

RESULT 3
US-08-652-816A-14
; Sequence 14, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-652-816A-14

Query Match 100.0%; Score 96; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 GINWGGSTGYADSVKG 66

RESULT 4
US-08-545-809A-106
; Sequence 106, Application US/08545809A
; Patent No. 8096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasaku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-106

Query Match 100.0%; Score 96; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVKG 17
DB 69 GINWNGSGTGADSVKG 85

RESULT 5
US-09-515-697-106
Sequence 106, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,697
FILING DATE: 29-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809
FILING DATE: 27-MAR-1996
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-515-697-106

Query Match 100.0%; Score 96; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVKG 17
DB 69 GINWNGSGTGADSVKG 85

RESULT 6
US-09-079-029-9
Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-9

Query Match: 100.0%; Score 96; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVKG 17
DB 89 GINWNGSGTGADSVKG 105

```
RESULT 7
US-09-424-840B-109
; Sequence 109, Application US/09424840B
; Patent No. 6790338
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-109

Query Match      82.3%; Score 79; DB 2; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.7e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
   ||| ||| ||| ||| |||
Db 1 GISWNSGSGYADSVKG 17

RESULT 8
US-09-534-717-598
; Sequence 598, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 598
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-598

Query Match      82.3%; Score 79; DB 2; Length 98;
Best Local Similarity 82.4%; Pred. No. 0.00052;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
   ||| ||| ||| ||| |||
Db 50 GISWNSGSGYADSVKG 66

RESULT 9
US-10-194-975-16
; Sequence 16, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
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; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-16

Query Match      82.3%; Score 79; DB 2; Length 99;
Best Local Similarity 82.4%; Pred. No. 0.00053;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
   ||| ||| ||| ||| |||
Db 50 GISWNSGSGYADSVKG 66

RESULT 10
US-08-545-809A-97
; Sequence 97, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Mateuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-97

Query Match      82.3%; Score 79; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00063;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
   ||| ||| ||| ||| |||
Db 69 GISWNSGSGYADSVKG 85
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RESULT 11
US-09-515-697-97
; Sequence 97, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; Matsuda, Humihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-Feb-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-515-697-97

Query Match 82.3%; Score 79; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00063;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
Db 69 GISWNSGSGIGYADSVK 85

RESULT 12
US-09-840-459-88
; Sequence 88, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537

; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-88

Query Match 82.3%; Score 79; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00064;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
Db 50 GISWNSGSGIGYADSVK 66

RESULT 13
US-09-497-625A-88
; Sequence 88, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-88

Query Match 82.3%; Score 79; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00064;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
Db 50 GISWNSGSGIGYADSVK 66

RESULT 14
US-08-958-201-8
; Sequence 8, Application US/08958201
; Patent No. 5977319
; GENERAL INFORMATION:
; APPLICANT: Pope, Anthony R.
; APPLICANT: Pritchard, Kevin
; APPLICANT: Williams, Andrew J.
; APPLICANT: Johnson, Kevin S.
; TITLE OF INVENTION: Specific binding members for estradiol;
; TITLE OF INVENTION: materials and methods
; NUMBER OF SEQUENCES: 23

; Patent No. 6914128

Best Local Similarity 81.2%; Pred. No. 0.007;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 INWNGSGTGYADSVKG 17
Db 51 ISWDGGSTYYADSVKG 66

RESULT 22

US-10-194-975-27
; Sequence 27, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-27

Query Match 74.0%; Score 71; DB 2; Length 99;
Best Local Similarity 81.2%; Pred. No. 0.007;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 INWNGSGTGYADSVKG 17
Db 51 ISWDGGSTYYADSVKG 66

RESULT 23

US-08-545-809A-119
; Sequence 119, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-119

Query Match 74.0%; Score 71; DB 2; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.0083;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
Db 69 GVSWSNGSRTHYADSVKG 85

RESULT 24

US-09-515-697-119
; Sequence 119, Application US/09515697
; Patent No. 6936705
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-Feb-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-09-515-697-119

Query Match 74.0%; Score 71; DB 2; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.0083;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17
Db 69 GVSWSNGSRTHYADSVKG 85

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;
; OPERATING SYSTEM: Windows95
; SOFTWARE: FabSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/515,697
; FILING DATE: 29-Feb-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809
; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 125:
;
; US-09-515-697-125
;
; Query Match 74.0%; Score 71; DB 2; Length 118;
; Best Local Similarity 81.2%; Pred. No. 0.0084;
; Matches 13; Conservative 2; Mismatches 1; Indels
;
; QY 2 INWNGSGTGYADSVKG 17
; Db :|:|||||
; 70 ISWDGSGTYYADSVKG 85
;
; RESULT 27
; US-09-424-840B-18
; Sequence 18, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-18
;
; Query Match 74.0%; Score 71; DB 2; Length 124;
; Best Local Similarity 70.6%; Pred. No. 0.0089;
; Matches 12; Conservative 3; Mismatches 2; Indels
;
; QY 1 GINWNGSGTGYADSVKG 17
; Db :|:|||||
; 50 GISWDGSGTGYADSVKG 66
;
; RESULT 28
; US-07-942-245-24
; Sequence 24, Application US/07942245

```

; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-24

Query Match 70.8%; Score 68; DB 1; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.022;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
Db 50 GISWSSSIGYADSVK 66

RESULT 29
US-09-232-290-35
; Sequence 35, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; PRIOR FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230
; PRIOR FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-232-290-35

Query Match 70.8%; Score 68; DB 2; Length 126;
Best Local Similarity 70.6%; Pred. No. 0.024;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
Db 50 GISWSSSIGYADSVK 66

RESULT 30
US-09-424-840B-70
; Sequence 70, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-05-08
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-70

Query Match 68.8%; Score 66; DB 2; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.0058;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
Db 1 GISWSTSIGYADSVK 17

RESULT 31
US-09-424-840B-78
; Sequence 78, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-05-08
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-78

Query Match 68.8%; Score 66; DB 2; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.0058;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSTGYADSVK 17
Db 1 GISWSTSIGYADSVK 17

Mon Nov 21 12:46:07 2005

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; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: FUSE5 fusion phase construct
; CLONE: Z78
; FEATURE:
; NAME/KEY: heavy chain
; US-08-983-607-26
;
Query Match 65.6%; Score 63; DB 2; Length 126;
Best Local Similarity 81.2%; Pred. No. 0.12;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 INWNGSGTGYADSVKG 17
Db 51 ISGNGSGTGYADSVKG 66

RESULT 34
US-09-157-370-1
; Sequence 1, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIFE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-157-370-1

Query Match 65.1%; Score 62.5; DB 2; Length 117;
Best Local Similarity 59.1%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17
Db 44 GLEWVGWIYNGDYYADSVKG 65

RESULT 35
US-08-264-093-22
; Sequence 22, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26

```

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RESULT 32
US-09-424-840B-123
; Sequence 123, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter F. A.
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-424-840B-123

Query Match 68.8%; Score 66; DB 2; Length 124;
Best Local Similarity 70.6%; Pred. No. 0.045;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
Db 50 GISWDSTSGYADSVKG 66

RESULT 33
US-08-983-607-26
; Sequence 26, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183

```

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ridout & Maybee
/ STREET: 2300 Richmond-Adelaide Centre
/ STREET: 101 Richmond Street West
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5H 2J7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: MS-DOS 6.00
/ SOFTWARE: ASCII Editor
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/264,093
/ FILING DATE:
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA: No. 5639863 applicable
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lake, James R.
/ REGISTRATION NUMBER: 31081
/ REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 868-1482
/ TELEFAX: (416) 362-0823
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not applicable
/ TOPOLOGY: linear
/ US-08-264-093-22

Query Match 64.6%; Score 62; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 0.021;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 INWGGSTGYADSVKG 17
|:|||||
Db 2 ISNNGGSTYYPDSVKG 17

RESULT 36
US-09-840-459-48
/ Sequence 48, Application US/09840459
/ Patent No. 6695550
/ GENERAL INFORMATION:
/ APPLICANT: LaRosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-012
/ CURRENT APPLICATION NUMBER: US/09/840,459
/ CURRENT FILING DATE: 2001-02-02
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: PCT/US01/03537
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: US/497,625
/ PRIOR FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 48
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ US-09-840-459-48

Query Match 64.6%; Score 62; DB 2; Length 89;
Best Local Similarity 81.2%; Pred. No. 0.12;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 INWGGSTGYADSVKG 17
|:|||||
Db 42 INSGGSTYYPDSVKG 57

RESULT 37
US-09-497-625A-48
/ Sequence 48, Application US/09497625A
/ Patent No. 6727349
/ GENERAL INFORMATION:
/ APPLICANT: LaRosa, Gregory J.
/ APPLICANT: Horvath, Christopher
/ APPLICANT: Newman, Walter
/ APPLICANT: Jones, S. Tarran
/ APPLICANT: O'Brien, Siobhan H.
/ APPLICANT: O'Keefe, Theresa
/ TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
/ METHODS OF USE THEREFOR
/ FILE REFERENCE: 1855.1052-004
/ CURRENT APPLICATION NUMBER: US/09/497,625A
/ CURRENT FILING DATE: 2000-02-03
/ PRIOR APPLICATION NUMBER: 09/359,193
/ PRIOR FILING DATE: 1999-07-22
/ PRIOR APPLICATION NUMBER: 09/121,781
/ PRIOR FILING DATE: 1998-07-23
/ NUMBER OF SEQ ID NOS: 106
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 48
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ US-09-497-625A-48

Query Match 64.6%; Score 62; DB 2; Length 89;
Best Local Similarity 81.2%; Pred. No. 0.12;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 INWGGSTGYADSVKG 17
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Db 42 INSGGSTYYPDSVKG 57

RESULT 38
US-09-534-717-620
/ Sequence 620, Application US/09534717
/ Patent No. 6914128
/ GENERAL INFORMATION:
/ APPLICANT: Jochen, Salfeld et al.
/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CP
/ CURRENT APPLICATION NUMBER: US/09/534,717
/ CURRENT FILING DATE: 2000-03-24
/ EARLIER APPLICATION NUMBER: 60/126,603
/ EARLIER FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 620
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-534-717-620

Query Match 64.6%; Score 62; DB 2; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 INWGGSTGYADSVKG 17
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Mon Nov 21 12:46:07 2005

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Db      51 ISSNGGTTYADSVKG 66

RESULT 39
US-09-534-717-621
; Sequence 621, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 621
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-621

Query Match      64.6%; Score 62; DB 2; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 INWNGGSGTYADSVKG 17
      |: ||||| |||||
Db      51 ISSNGGTTYADSVKG 66

RESULT 40
US-09-534-717-633
; Sequence 633, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 633
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-633

Query Match      64.6%; Score 62; DB 2; Length 98;
Best Local Similarity 81.2%; Pred. No. 0.13;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 INWNGGSGTYADSVKG 17
      |: ||||| |||||
Db      51 ISSNGGTTYADSVKG 66

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Job time : 55.0357 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:14:46 ; Search time 182.75 Seconds
(without alignments)
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Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSGTGYADSVKG 17

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA Main:*

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6: /cgn2_6/prodata/1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	96	100.0	17	4	US-10-029-988B-115
3	96	100.0	17	4	US-10-032-423A-115
4	96	100.0	17	4	US-10-029-926B-115
5	96	100.0	98	4	US-10-194-975-20
6	96	100.0	98	4	US-10-308-817-60
7	96	100.0	98	4	US-10-032-037B-61
8	96	100.0	98	4	US-10-029-988B-61
9	96	100.0	98	4	US-10-032-423A-61
10	96	100.0	98	4	US-10-453-698-60
11	96	100.0	98	4	US-10-029-926B-61
12	96	100.0	98	4	US-10-379-392-21
13	96	100.0	98	5	US-10-884-830-599
14	96	100.0	122	6	US-10-447-331-6
15	96	100.0	123	6	US-11-039-767-12
16	96	100.0	146	5	US-10-909-851-29
17	96	100.0	239	3	US-09-880-748-937
18	96	100.0	239	3	US-09-880-748-2015
19	96	100.0	239	3	US-09-880-748-2038
20	96	100.0	239	4	US-10-293-418-937
21	96	100.0	239	4	US-10-293-418-2015
22	96	100.0	239	4	US-10-293-418-2038
23	96	100.0	242	5	US-10-935-290-130
24	96	100.0	242	6	US-11-017-030-28
25	96	100.0	244	4	US-10-322-673-42
26	96	100.0	244	5	US-10-981-465-42
27	96	100.0	244	5	US-10-981-621-42

28	96	100.0	244	5	US-10-981-673-42	Sequence 42, Appl
29	96	100.0	244	5	US-10-981-691-42	Sequence 40, Appl
30	96	100.0	249	5	US-10-935-290-40	Sequence 42, Appl
31	96	100.0	266	4	US-10-032-037B-204	Sequence 204, Appl
32	96	100.0	266	4	US-10-029-988B-204	Sequence 204, Appl
33	96	100.0	266	4	US-10-032-423A-204	Sequence 204, Appl
34	96	100.0	277	4	US-10-032-037B-25	Sequence 25, Appl
35	96	100.0	277	4	US-10-032-037B-203	Sequence 203, Appl
36	96	100.0	277	4	US-10-029-988B-25	Sequence 25, Appl
37	96	100.0	277	4	US-10-029-988B-203	Sequence 203, Appl
38	96	100.0	277	4	US-10-032-423A-25	Sequence 25, Appl
39	96	100.0	277	4	US-10-032-423A-203	Sequence 203, Appl
40	96	100.0	277	4	US-10-029-926B-25	Sequence 25, Appl
41	96	100.0	277	4	US-10-029-926B-203	Sequence 203, Appl
42	96	100.0	277	4	US-10-610-843B-1	Sequence 1, Appl
43	96	100.0	278	4	US-10-610-843B-2	Sequence 2, Appl
44	96	100.0	280	4	US-10-610-843B-3	Sequence 3, Appl
45	96	100.0	280	4	US-10-611-588C-1	Sequence 1, Appl
46	96	100.0	280	5	US-10-880-922-5	Sequence 5, Appl
47	96	100.0	280	5	US-10-880-922-6	Sequence 6, Appl
48	96	100.0	280	5	US-10-880-922-55	Sequence 55, Appl
49	96	100.0	280	5	US-10-880-922-56	Sequence 56, Appl
50	96	100.0	280	5	US-10-880-922-60	Sequence 60, Appl
51	96	100.0	280	5	US-10-880-922-61	Sequence 61, Appl
52	96	100.0	309	4	US-10-052-798-9	Sequence 9, Appl
53	96	100.0	309	4	US-10-288-917-9	Sequence 9, Appl
54	96	100.0	309	4	US-10-423-448-9	Sequence 9, Appl
55	96	100.0	464	4	US-10-032-037B-26	Sequence 26, Appl
56	96	100.0	464	4	US-10-029-988B-26	Sequence 26, Appl
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58	96	100.0	464	4	US-10-029-926B-26	Sequence 26, Appl
59	90	93.8	16	4	US-10-610-843B-5	Sequence 5, Appl
60	90	93.8	16	4	US-10-611-588C-3	Sequence 3, Appl
61	90	93.8	16	5	US-10-880-922-17	Sequence 17, Appl
62	90	93.8	17	5	US-10-891-658-117	Sequence 117, Appl
63	90	93.8	17	5	US-10-989-462-71	Sequence 71, Appl
64	90	93.8	124	5	US-10-891-658-87	Sequence 87, Appl
65	90	93.8	128	5	US-10-989-462-9	Sequence 9, Appl
66	90	93.8	263	5	US-10-989-462-35	Sequence 35, Appl
67	79	82.3	17	4	US-10-844-424-109	Sequence 109, Appl
68	79	82.3	98	4	US-10-032-037B-60	Sequence 60, Appl
69	79	82.3	98	4	US-10-029-988B-60	Sequence 60, Appl
70	79	82.3	98	4	US-10-032-423A-60	Sequence 60, Appl
71	79	82.3	98	4	US-10-029-926B-60	Sequence 60, Appl
72	79	82.3	99	4	US-10-884-830-598	Sequence 598, Appl
73	79	82.3	99	4	US-10-194-975-16	Sequence 16, Appl
74	79	82.3	99	4	US-10-308-817-56	Sequence 56, Appl
75	79	82.3	99	4	US-10-453-698-56	Sequence 56, Appl
76	79	82.3	99	4	US-10-379-392-15	Sequence 15, Appl
77	79	82.3	117	6	US-11-021-438-4	Sequence 4, Appl
78	79	82.3	119	4	US-09-840-459-88	Sequence 88, Appl
79	79	82.3	119	4	US-10-766-773-88	Sequence 88, Appl
80	79	82.3	119	4	US-10-766-610-88	Sequence 88, Appl
81	79	82.3	119	4	US-10-733-563-88	Sequence 88, Appl
82	79	82.3	120	5	US-10-487-525-1	Sequence 1, Appl
83	79	82.3	120	6	US-11-039-767-16	Sequence 16, Appl
84	79	82.3	122	6	US-11-021-438-2	Sequence 2, Appl
85	79	82.3	127	4	US-10-466-242-7	Sequence 7, Appl
86	79	82.3	132	3	US-09-791-153A-65	Sequence 65, Appl
87	79	82.3	141	6	US-10-687-799-56	Sequence 56, Appl
88	79	82.3	241	6	US-11-021-438-24	Sequence 24, Appl
89	79	82.3	244	5	US-10-981-692-26	Sequence 26, Appl
90	79	82.3	245	6	US-11-021-438-22	Sequence 22, Appl
91	79	82.3	254	3	US-09-880-748-1427	Sequence 1427, Ap
92	79	82.3	254	4	US-10-293-418-1427	Sequence 1427, Ap
93	79	82.3	291	4	US-10-406-830-6	Sequence 6, Appl
94	78	81.2	109	3	US-10-387-955-74	Sequence 74, Appl
95	76	79.2	109	3	US-09-864-408A-6842	Sequence 6842, Ap
96	76	79.2	245	3	US-09-880-748-1926	Sequence 1926, Ap
97	76	79.2	245	4	US-10-293-418-1926	Sequence 1926, Ap
98	75	78.1	241	2	US-08-779-457-50	Sequence 50, Appl
99	75	78.1	241	5	US-10-921-710-50	Sequence 50, Appl
100	74	77.1	17	3	US-09-791-153A-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-10-032-037B-115
; Sequence 115, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-115

Query Match      100.0%; Score 96; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGADSVK 17
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Db      1 GINWNGSGTGADSVK 17

RESULT 2
US-10-029-988B-115
; Sequence 115, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/46
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-115

Query Match      100.0%; Score 96; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGADSVK 17
      |||||
Db      1 GINWNGSGTGADSVK 17

RESULT 3
US-10-032-423A-115
; Sequence 115, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/45
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-115

Query Match      100.0%; Score 96; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGADSVK 17
      |||||
Db      1 GINWNGSGTGADSVK 17

RESULT 4
US-10-029-926B-115
; Sequence 115, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-115

Query Match      100.0%; Score 96; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GINWNGSGTGADSVK 17
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Db      1 GINWNGSGTGADSVK 17

RESULT 5
US-10-194-975-20
; Sequence 20, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-20

Query Match      100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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RESULT 8
 US-10-029-988B-61
 ; Sequence 61, Application US/10029988B
 ; Publication No. US20040001839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bio-Technology General Corp.
 ; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

Query Match 100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels

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Qy 1 GINWGGSTGYADSVKG 17
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Db 50 GINWGGSTGYADSVKG 66

RESULT 11
US-10-029-926B-61
; Sequence 61, Application US/10029926B
; Publication No. US2004007301A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-61

Query Match 100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
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Db 50 GINWGGSTGYADSVKG 66

RESULT 12
US-10-379-392-21
; Sequence 21, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-21

Query Match 100.0%; Score 96; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
|||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 13
US-10-884-830-599
; Sequence 599, Application US/10884830
; Publication No. US20050004354A1
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; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BEI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-599

Query Match 100.0%; Score 96; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
|||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 14
US-10-447-331-6
; Sequence 6, Application US/10447331
; Publication No. US20030219434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-6

Query Match 100.0%; Score 96; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
|||||
Db 50 GINWGGSTGYADSVKG 66

RESULT 15
US-11-039-767-12
; Sequence 12, Application US/11039767
; Publication No. US20050170398A1
; GENERAL INFORMATION:
; APPLICANT: CRUCELL HOLLAND B.V.
; TITLE OF INVENTION: Recombinant production of mixtures of antibodies
; FILE REFERENCE: 0079 WO 00 ORD
; CURRENT APPLICATION NUMBER: US/11/039,767
; CURRENT FILING DATE: 2005-01-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
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; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH sequence of clone B28 (anti-CD22 phase)
US-11-039-767-12

Query Match          100.0%; Score 96; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.5e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 GINWNGSGTGADSVKG 17
Db 52 GINWNGSGTGADSVKG 68

RESULT 16
US-10-909-851-29
; Sequence 29, Application US/10909851
; Publication No. US20050170334A1
; GENERAL INFORMATION:
; APPLICANT: Kirin Brewery Co.
; APPLICANT: Mikayama, Toshifumi
; APPLICANT: Wang, Rongfang
; APPLICANT: Kato, Shinichiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INFLUENZA M2 PROTEIN AND METHODS
; TITLE OF INVENTION: AND USING SAME
; FILE REFERENCE: 021286-0309187
; CURRENT APPLICATION NUMBER: US/10/909,851
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: 60/364,997
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 10/389,221
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: PCT/US03/08147
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-851-29

Query Match          100.0%; Score 96; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 5.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 GINWNGSGTGADSVKG 17
Db 69 GINWNGSGTGADSVKG 85

RESULT 17
US-09-880-748-937
; Sequence 937, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
```

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; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-937

Query Match          100.0%; Score 96; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 GINWNGSGTGADSVKG 17
Db 50 GINWNGSGTGADSVKG 66

RESULT 18
US-09-880-748-2015
; Sequence 2015, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2015
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2015

Query Match          100.0%; Score 96; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 GINWNGSGTGADSVKG 17
Db 50 GINWNGSGTGADSVKG 66

RESULT 19
US-09-880-748-2038
; Sequence 2038, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
```

```
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2038

Query Match      100.0%; Score 96; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
   |||||
Db 50 GINWNGGSTGYADSVKG 66

RESULT 20
US-10-293-418-937
; Sequence 937, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match      100.0%; Score 96; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
   |||||
Db 50 GINWNGGSTGYADSVKG 66

RESULT 21
US-10-293-418-2015
; Sequence 2015, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 937
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-937

Query Match      100.0%; Score 96; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
   |||||
Db 50 GINWNGGSTGYADSVKG 66

RESULT 22
US-10-293-418-2038
; Sequence 2038, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2038
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2038

Query Match      100.0%; Score 96; DB 4; Length 239;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
   |||||
Db 50 GINWNGGSTGYADSVKG 66

RESULT 23
US-10-935-290-130
```

; Sequence 130, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PF584P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 130
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMCC127
US-10-935-290-130

Query Match 100.0%; Score 96; DB 5; Length 242;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
|||
DB 50 GINWNGSGTGADSVK 66

RESULT 24

US-11-017-030-28
; Sequence 28, Application US/11017030
; Publication No. US20050158313A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Reg IV
; FILE REFERENCE: PF592PCT
; CURRENT APPLICATION NUMBER: US/11/017,030
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: PCT/US03/19908
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 60/392,382
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: scFv protein RGC0115
US-11-017-030-28

Query Match 100.0%; Score 96; DB 6; Length 242;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
|||
DB 50 GINWNGSGTGADSVK 66

RESULT 25

US-10-322-673-42
; Sequence 42, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673

; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-322-673-42

Query Match 100.0%; Score 96; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 17
|||
DB 50 GINWNGSGTGADSVK 66

RESULT 26

US-10-981-465-42
; Sequence 42, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1
; CURRENT APPLICATION NUMBER: US/10/981,465
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-465-42

Query Match 100.0%; Score 96; DB 5; Length 244;

Best Local Similarity 100.0%; Pred. No. 9e-06; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

Qy 1 GINWGGSTGYADSVK 17
Db 50 GINWGGSTGYADSVK 66

RESULT 27

US-10-981-621-42
; Sequence 42, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-621-42

Query Match 100.0%; Score 96; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVK 17
Db 50 GINWGGSTGYADSVK 66

RESULT 28

US-10-981-673-42
; Sequence 42, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05

; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-673-42

Query Match 100.0%; Score 96; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVK 17
Db 50 GINWGGSTGYADSVK 66

RESULT 29

US-10-981-691-42
; Sequence 42, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID3
; CURRENT APPLICATION NUMBER: US/10/981,691
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 42
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM005G08 scFv
US-10-981-621-42

; OTHER INFORMATION: CM005G08 SCFV
US-10-981-691-42

```
Query Match      100.0%; Score 96; DB 5; Length 244;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GINWNGGSTGYADSVKG 17
|||
Db 50 GINWNGGSTGYADSVKG 66

```

RESULT 30
US-10-935-290-40
; Sequence 40, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GNAID
; FILE REFERENCE: PF584P1
; CURRENT APPLICATION NUMBER: US/10/935.290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 40
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMB6C603
US-10-935-290-40

```

```
Query Match      100.0%; Score 96; DB 5; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GINWNGGSTGYADSVKG 17
|||
Db 50 GINWNGGSTGYADSVKG 66

```

RESULT 31
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: V17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOITIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

```

Query Match	100.0%;	Score 96;	DB 4;	Length 266;
Best Local Similarity	100.0%;	Pred. No. 9.8e-06;		
Matches 17:	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

Qy 1 GINWNGGSTGYADSVKG 17
|||
pb 72 GINWNGGSTGYADSVKG 88

```

RESULT 32
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

```

```
Query Match      100.0%; Score 96; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GINWNGSGYADSVKG 17
|||
Db 72 GINWNGSGYADSVKG 88

```

RESULT 33
US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF.
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

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Query Match      100.0%; Score 96; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GINWGGSTGYADSVKG 17
|||
nb 72 GINWGGSTGYADSVKG 88

RESULT 34. .
US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948

1 PRIOR FILING DATE: 2000-12-29
2 NUMBER OF SEQ ID NOS: 204
3 SOFTWARE: FastSeq for Windows Version 3.0
4 SEQ ID NO 25
5 LENGTH: 277
6 TYPE: PRT
7 ORGANISM: Homo sapiens
8 US-10-032-037B-25

Query Match 100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
Db 72 GINWNGGSTGYADSVKG 88

RESULT 35

US-10-032-037B-203
Sequence 203, Application US/10032037B
Publication No. US20040001822A1

GENERAL INFORMATION:

1 APPLICANT: Bio-Technology General Corp.
2 TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
3 MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
4 FILE REFERENCE: 10793/44
5 CURRENT APPLICATION NUMBER: US/10/032,037B
6 PRIOR FILING DATE: 2001-12-31
7 PRIOR APPLICATION NUMBER: 60/258,948
8 PRIOR FILING DATE: 2000-12-29
9 NUMBER OF SEQ ID NOS: 204
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 203
12 LENGTH: 277
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 US-10-032-037B-203

Query Match 100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
Db 72 GINWNGGSTGYADSVKG 88

RESULT 36

US-10-029-988B-25
Sequence 25, Application US/10029988B
Publication No. US20040001839A1

GENERAL INFORMATION:

1 APPLICANT: Bio-Technology General Corp.
2 TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
3 MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
4 FILE REFERENCE: 10793/46
5 CURRENT APPLICATION NUMBER: US/10/029,988B
6 PRIOR FILING DATE: 2001-12-31
7 PRIOR APPLICATION NUMBER: 60/258,948
8 PRIOR FILING DATE: 2000-12-29
9 NUMBER OF SEQ ID NOS: 204
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 25
12 LENGTH: 277
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 US-10-029-988B-25

Query Match 100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
Db 72 GINWNGGSTGYADSVKG 88

RESULT 37

US-10-029-988B-203
Sequence 203, Application US/10029988B
Publication No. US20040001839A1

GENERAL INFORMATION:

1 APPLICANT: Bio-Technology General Corp.
2 TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
3 MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
4 FILE REFERENCE: 10793/46
5 CURRENT APPLICATION NUMBER: US/10/029,988B
6 PRIOR FILING DATE: 2001-12-31
7 PRIOR APPLICATION NUMBER: 60/258,948
8 PRIOR FILING DATE: 2000-12-29
9 NUMBER OF SEQ ID NOS: 204
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 203
12 LENGTH: 277
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 US-10-029-988B-203

Query Match 100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
Db 72 GINWNGGSTGYADSVKG 88

RESULT 38

US-10-032-423A-25
Sequence 25, Application US/10032423A
Publication No. US20040002450A1

GENERAL INFORMATION:

1 APPLICANT: Bio-Technology General Corp.
2 TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
3 MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
4 FILE REFERENCE: 10793/45
5 CURRENT APPLICATION NUMBER: US/10/032,423A
6 CURRENT FILING DATE: 2001-12-31
7 PRIOR APPLICATION NUMBER: 60/258,948
8 PRIOR FILING DATE: 12/29/2000
9 NUMBER OF SEQ ID NOS: 204
10 SOFTWARE: FastSeq for Windows Version 3.0
11 SEQ ID NO 25
12 LENGTH: 277
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 US-10-032-423A-25

Query Match 100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GINWNGGSTGYADSVKG 17
Db 72 GINWNGGSTGYADSVKG 88

RESULT 39

US-10-032-423A-203
Sequence 203, Application US/10032423A
Publication No. US20040002450A1

GENERAL INFORMATION:

1 APPLICANT: Bio-Technology General Corp.
2 TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
3 MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

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; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203
```

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Query Match      100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GINWNGGSGYADSVKG 17
          |||||
Db      72 GINWNGGSGYADSVKG 88
```

```
RESULT 40
US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25
```

```
Query Match      100.0%; Score 96; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GINWNGGSGYADSVKG 17
          |||||
Db      72 GINWNGGSGYADSVKG 88
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Search completed: November 18, 2005, 21:40:05
Job time : 183.75 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:15:38 ; Search time 4.85714 Seconds
(without alignments)
3.954 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSGTGVADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
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- 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	65.6	122	7	US-11-144-248-24
2	61	63.5	98	1	US-10-789-273-10
3	61	63.5	98	7	US-11-144-248-32
4	61	63.5	121	1	US-10-789-273-9
5	61	63.5	470	7	US-11-144-248-46
6	58	60.4	124	7	US-11-144-248-8
7	58	60.4	470	7	US-11-144-248-45
8	55	57.3	123	7	US-11-144-248-16
9	55	57.3	139	1	US-10-721-763-33
10	49	51.0	120	7	US-11-077-978-7
11	49	51.0	138	1	US-10-789-273-8
12	49	51.0	138	1	US-10-789-273-12
13	48	50.0	174	7	US-11-144-248-4
14	48	50.0	252	1	US-10-512-184-28
15	48	50.0	470	7	US-11-144-248-49
16	46	47.9	98	7	US-11-144-248-30
17	46	47.9	102	1	US-10-997-201A-6
18	46	47.9	121	7	US-11-077-978-2
19	46	47.9	473	7	US-11-144-248-50
20	45	46.9	250	1	US-10-512-184-27
21	45	46.9	444	7	US-11-172-320-6
22	44	45.8	138	1	US-10-789-273-4
23	44	45.8	258	1	US-10-512-184-26
24	44	45.8	327	1	US-10-512-184-62
25	44	45.8	327	1	US-10-512-184-64
26	44	45.8	327	1	US-10-512-184-64
27	44	45.8	327	1	US-10-512-184-64
28	44	45.8	327	1	US-10-512-184-64
29	44	45.8	327	1	US-10-512-184-64
30	44	45.8	327	1	US-10-512-184-64
31	44	45.8	327	1	US-10-512-184-64
32	44	45.8	327	1	US-10-512-184-64
33	44	45.8	327	1	US-10-512-184-64
34	44	45.8	327	1	US-10-512-184-64
35	44	45.8	327	1	US-10-512-184-64
36	44	45.8	327	1	US-10-512-184-64
37	44	45.8	327	1	US-10-512-184-64
38	44	45.8	327	1	US-10-512-184-64
39	44	45.8	327	1	US-10-512-184-64
40	44	45.8	327	1	US-10-512-184-64
41	44	45.8	327	1	US-10-512-184-64
42	44	45.8	327	1	US-10-512-184-64
43	44	45.8	327	1	US-10-512-184-64
44	44	45.8	327	1	US-10-512-184-64
45	44	45.8	327	1	US-10-512-184-64
46	44	45.8	327	1	US-10-512-184-64
47	44	45.8	327	1	US-10-512-184-64
48	44	45.8	327	1	US-10-512-184-64
49	44	45.8	327	1	US-10-512-184-64
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51	44	45.8	327	1	US-10-512-184-64
52	44	45.8	327	1	US-10-512-184-64
53	44	45.8	327	1	US-10-512-184-64
54	44	45.8	327	1	US-10-512-184-64
55	44	45.8	327	1	US-10-512-184-64
56	44	45.8	327	1	US-10-512-184-64
57	44	45.8	327	1	US-10-512-184-64
58	44	45.8	327	1	US-10-512-184-64
59	44	45.8	327	1	US-10-512-184-64
60	44	45.8	327	1	US-10-512-184-64
61	44	45.8	327	1	US-10-512-184-64
62	44	45.8	327	1	US-10-512-184-64
63	44	45.8	327	1	US-10-512-184-64
64	44	45.8	327	1	US-10-512-184-64
65	44	45.8	327	1	US-10-512-184-64
66	44	45.8	327	1	US-10-512-184-64
67	44	45.8	327	1	US-10-512-184-64
68	44	45.8	327	1	US-10-512-184-64
69	44	45.8	327	1	US-10-512-184-64
70	44	45.8	327	1	US-10-512-184-64
71	44	45.8	327	1	US-10-512-184-64
72	44	45.8	327	1	US-10-512-184-64
73	44	45.8	327	1	US-10-512-184-64
74	44	45.8	327	1	US-10-512-184-64
75	44	45.8	327	1	US-10-512-184-64
76	44	45.8	327	1	US-10-512-184-64
77	44	45.8	327	1	US-10-512-184-64
78	44	45.8	327	1	US-10-512-184-64
79	44	45.8	327	1	US-10-512-184-64
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83	44	45.8	327	1	US-10-512-184-64
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85	44	45.8	327	1	US-10-512-184-64
86	44	45.8	327	1	US-10-512-184-64
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92	44	45.8	327	1	US-10-512-184-64
93	44	45.8	327	1	US-10-512-184-64
94	44	45.8	327	1	US-10-512-184-64
95	44	45.8	327	1	US-10-512-184-64
96	44	45.8	327	1	US-10-512-184-64
97	44	45.8	327	1	US-10-512-184-64
98	44	45.8	327	1	US-10-512-184-64

Sequence 63, Appl
Sequence 65, Appl
Sequence 47, Appl
Sequence 8, Appl
Sequence 25, Appl
Sequence 74, Appl
Sequence 80, Appl
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Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
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Sequence 3, Appl
Sequence 36, Appl
Sequence 44, Appl
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Sequence 20, Appl
Sequence 47, Appl
Sequence 5, Appl
Sequence 15, Appl
Sequence 38, Appl
Sequence 72, Appl
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Sequence 21, Appl
Sequence 13, Appl
Sequence 76, Appl
Sequence 78, Appl
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Sequence 74, Appl
Sequence 17, Appl
Sequence 25, Appl
Sequence 4, Appl
Sequence 33, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 306, App
Sequence 18, Appl
Sequence 472, App
Sequence 4, Appl
Sequence 8, Appl
Sequence 330, App
Sequence 6, Appl
Sequence 136, App
Sequence 36, App
Sequence 60, App
Sequence 52, App
Sequence 166, App
Sequence 234, App
Sequence 254, App
Sequence 134, App
Sequence 12, App

99 32.5 33.9 117 7 US-11-012-353-75 Sequence 75, Appl
100 32.5 33.9 135 7 US-11-012-353-77 Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-11-144-248-24
; Sequence 24, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-24

Query Match 65.6%; Score 63; DB 7; Length 122;
Best Local Similarity 76.5%; Pred. No. 0.0009;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
| : ||||| |||||
Db 50 GITGGGSGTYADSVKG 66

RESULT 2
US-10-789-273-10
; Sequence 10, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-10

Query Match 63.5%; Score 61; DB 1; Length 98;
Best Local Similarity 56.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

Qy 1 GINW-----NGGSTGYADSVKG 17
| : ||||| |||||
Db 44 GLEWVSAISGGSGSTYYADSVKG 66

RESULT 3
US-11-144-248-32
; Sequence 32, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-32

Query Match 63.5%; Score 61; DB 7; Length 98;
Best Local Similarity 56.5%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

Qy 1 GINW-----NGGSTGYADSVKG 17
| : ||||| |||||
Db 44 GLEWVSAISGGSGSTYYADSVKG 66

RESULT 4
US-10-789-273-9
; Sequence 9, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-9

Query Match 63.5%; Score 61; DB 1; Length 121;
Best Local Similarity 56.5%; Pred. No. 0.0017;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GINW-----NGGSTGYADSVKG 17

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Db 44 GLEWVSAISGGGITYYADSVKG 66
RESULT 9
US-10-721-763-33
; Sequence 33, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 33
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-33
Query Match 57.3%; Score 55; DB 1; Length 139;
Best Local Similarity 52.2%; Pred. No. 0.015;
Matches 12; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
Qy 1 GINW-----NGGSTGYADSVKG 17
: : : : :
: : : : :
Db 63 GLEWVSAISGGGSRYYADSVKG 85
RESULT 10
US-11-077-978-7
; Sequence 7, Application US/11077978
; Publication No. US20050244333A1
; GENERAL INFORMATION:
; APPLICANT: Yazaki, Paul J.
; APPLICANT: Sherman, Mark A.
; APPLICANT: Shively, John E.
; APPLICANT: Raubitschek, Andrew A.
; APPLICANT: Wu, Anna M.
; TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
; FILE REFERENCE: 54435.8012.US01
; CURRENT APPLICATION NUMBER: US/11/077,978
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 7
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Variable heavy chain of humanized anti-p185HER2 antibody 4D5,
; US-11-077-978-7
Query Match 51.0%; Score 49; DB 7; Length 120;
Best Local Similarity 47.8%; Pred. No. 0.097;
Matches 11; Conservative 1; Mismatches 5; Indels 6; Gaps 1;
Qy 1 GINW-----NGGSTGYADSVKG 17
: : : : :
: : : : :
Db 44 GLEWVARIYPTNGTRYADSVKG 66
RESULT 11
US-10-789-273-8
; Sequence 8, Application US/10789273
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; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurik
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-789-273-8
Query Match 51.0%; Score 49; DB 1; Length 138;
Best Local Similarity 43.5%; Pred. No. 0.11;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;
Qy 1 GINW-----NGGSTGYADSVKG 17
: : : : :
: : : : :
Db 63 GLEWVASIRSGGRTYYSDNVKG 85
RESULT 12
US-10-789-273-12
; Sequence 12, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurik
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 light chain variable region
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-789-273-12
Query Match 51.0%; Score 49; DB 1; Length 138;
Best Local Similarity 43.5%; Pred. No. 0.11;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;
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RESULT 17
US-10-997-201A-6
; Sequence 6, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-6

Query Match          47.9%; Score 46; DB 1; Length 102;
Best Local Similarity 52.9%; Pred. No. 0.23;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GINWGGSTGYADSVKG 17
   | : | : | : | : | : |
Db 40 GLEWVISGYYADSVKG 56

RESULT 18
US-11-077-978-2
; Sequence 2, Application US/11077978
; Publication No. US20050244333A1
; GENERAL INFORMATION:
; APPLICANT: Yazaki, Paul J.
; APPLICANT: Sherman, Mark A.
; APPLICANT: Shively, John E.
; APPLICANT: Raubitschek, Andrew A.
; APPLICANT: Wu, Anna M.
; TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
; FILE REFERENCE: 54435.8012.US01
; CURRENT APPLICATION NUMBER: US/11/077,978
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially constructed variable heavy chain of MSA humanized
; OTHER INFORMATION: antibody
US-11-077-978-2

Query Match          47.9%; Score 46; DB 7; Length 121;
Best Local Similarity 43.5%; Pred. No. 0.27;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

Qy 1 GINW-----NGSGTGYADSVKG 17
   | : | : | : | : | : |
Db 44 GLEWVARIDPANGSKYADSVKG 66

RESULT 19
US-11-144-248-50
; Sequence 50, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; FILE REFERENCE: 1/1383
```

```
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-50

Query Match          47.9%; Score 46; DB 7; Length 473;
Best Local Similarity 43.5%; Pred. No. 0.96;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

Qy 1 GINW-----NGSGTGYADSVKG 17
   | : | : | : | : | : |
Db 63 GLEWVSYISSGSGTYYADSVKG 85

RESULT 20
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match          46.9%; Score 45; DB 1; Length 250;
Best Local Similarity 47.8%; Pred. No. 0.74;
Matches 11; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

Qy 1 GINW-----NGGS-TGYADSVKG 17
   | : | : | : | : | : |
Db 46 GLEWVAGIDGGSFTGYGAADVKG 68

RESULT 21
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
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RESULT 23
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US2005024901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft
; TITLE OF INVENTION: Antibodies, rec:

```

US-10-512-184-64
; Sequence 64, Application US/10512184
; Publication No. US2005024901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft
; TITLE OF INVENTION: Antibodies, rec
; TITLE OF INVENTION: antibody fragm
; TITLE OF INVENTION: resistance aga
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/5
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1

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/ SEQ ID NO 64
/ LENGTH: 327
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: precursor
/ OTHER INFORMATION: fusion protein comprising lactoferricin - linker -
US-10-512-184-64
; OTHER INFORMATION: scFv CWP22.

Query Match          45.8%; Score 44; DB 1; Length 327;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVK 17
||: :| :| :| :|
Db 121 GISDGS DNTNYS AVKG 137

RESULT 26
US-10-512-184-63
; Sequence 63, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker -
; OTHER INFORMATION: scFv CWP22.
US-10-512-184-63

Query Match          45.8%; Score 44; DB 1; Length 328;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVK 17
||: :| :| :| :|
Db 122 GISDGS DNTNYS AVKG 138

RESULT 27
US-10-512-184-65
; Sequence 65, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising chitinase - linker -
; OTHER INFORMATION: scFv CWP22.

; OTHER INFORMATION: scFv CWP22.

Query Match          45.8%; Score 44; DB 1; Length 576;
Best Local Similarity 47.1%; Pred. No. 2.3;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVK 17
||: :| :| :| :|
Db 370 GISDGS DNTNYS AVKG 386

RESULT 28
US-10-512-184-47
; Sequence 47, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scFv CWP22 - cmcy/His6.
US-10-512-184-47

Query Match          45.8%; Score 44; DB 1; Length 625;
Best Local Similarity 47.1%; Pred. No. 2.4;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVK 17
||: :| :| :| :|
Db 393 GISDGS DNTNYS AVKG 409

RESULT 29
US-10-726-554-8
; Sequence 8, Application US/10726554
; Publication No. US20050249753A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
; TITLE OF INVENTION: THE HEV S-SURFACE
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,554
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US/09/865,483
; PRIOR FILING DATE: PRIORITY FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Escherichia coli
; OTHER INFORMATION: scFv CWP22.
US-10-726-554-8

Query Match          43.8%; Score 42; DB 1; Length 114;
Best Local Similarity 54.5%; Pred. No. 0.97;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGY 11
||: :| :| :| :|
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: VH7 heavy chain
US-11-174-186-18

Query Match 41.7%; Score 40; DB 7; Length 116;
Best Local Similarity 39.1%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

Qy 1 GINWNG-----GSTGYADSVKG 17
| : | | | | | | | | | |
Db 44 GLKWMGWINTYTGPTVADDFKG 66

RESULT 35

US-11-174-186-19
; Sequence 19, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: VH2.5 heavy chain
US-11-174-186-19

Query Match 41.7%; Score 40; DB 7; Length 116;
Best Local Similarity 39.1%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

Qy 1 GINWNG-----GSTGYADSVKG 17
| : | | | | | | | | | |
Db 44 GLKWMGWINTYTGPTVADDFKG 66

RESULT 36

US-11-174-186-20
; Sequence 20, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS VH veneered

US-11-174-186-20

Query Match 41.7%; Score 40; DB 7; Length 116;
Best Local Similarity 39.1%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

Qy 1 GINWNG-----GSTGYADSVKG 17
| : | | | | | | | | | |
Db 44 GLKWMGWINTYTGPTVADDFKG 66

RESULT 37

US-11-174-186-21
; Sequence 21, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS de-immunized VH1
US-11-174-186-21

Query Match 41.7%; Score 40; DB 7; Length 116;
Best Local Similarity 39.1%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

Qy 1 GINWNG-----GSTGYADSVKG 17
| : | | | | | | | | | |
Db 44 GLKWMGWINTYTGPTVADDFKG 66

RESULT 38

US-11-174-186-22
; Sequence 22, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22

Query Match 41.7%; Score 40; DB 7; Length 116;
Best Local Similarity 39.1%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 7; Indels 6; Gaps 1;

Qy 1 GINWNG-----GSTGYADSVKG 17

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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:58:55 ; Search time 35.2143 Seconds
(without alignments)
46.449 Million cell updates/sec

Title: US-10-029-926D-115
Perfect score: 96
Sequence: 1 GINWNGSGTGYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 80:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	98	2 S26928	Ig heavy chain V r
2	87	90.6	112	2 PH1654	Ig heavy chain V r
3	79	82.3	98	2 S26927	Ig heavy chain V r
4	79	82.3	121	2 S31104	Ig heavy chain (su
5	79	82.3	128	2 S31595	Ig heavy chain V r
6	76	79.2	123	2 S30332	Ig heavy chain V r
7	74	77.1	121	2 S31118	Ig heavy chain - h
8	73	76.0	100	2 S69896	Ig heavy chain V r
9	71	74.0	98	2 S26934	Ig heavy chain V r
10	71	74.0	98	2 S26929	Ig heavy chain V r
11	71	74.0	120	2 S44111	Ig heavy chain V-D
12	71	74.0	191	2 JLO048	Ig heavy chain V-I
13	69	71.9	120	1 GIH048	Ig heavy chain V r
14	68	70.8	145	2 S11239	Ig heavy chain V r
15	65	67.7	120	2 S36273	Ig heavy chain V r
16	65	67.7	123	2 PC4281	anti-SS-A/RO 60K p
17	64	66.7	90	2 S24248	Ig heavy chain V r
18	64	66.7	120	2 S36278	Ig heavy chain V r
19	62	64.6	96	2 S20781	Ig heavy chain V r
20	61.5	64.1	97	2 S26935	Ig heavy chain V r
21	61.5	64.1	97	2 S46462	Ig heavy chain V r
22	61.5	64.1	116	2 B28966	Ig heavy chain pre
23	61.5	64.1	116	2 S31110	Ig heavy chain - h
24	61.5	64.1	146	2 I47184	Ig heavy chain var
25	61	63.5	98	2 S26889	Ig heavy chain V r
26	61	63.5	98	2 S54856	Ig heavy chain V r
27	61	63.5	99	2 S24259	Ig heavy chain V r
28	61	63.5	100	2 S24258	Ig heavy chain V r
29	61	63.5	101	2 S24257	Ig heavy chain V r

30	61	63.5	102	2 S24260	Ig heavy chain V r
31	61	63.5	104	2 S24255	Ig heavy chain V r
32	61	63.5	105	2 S24249	Ig heavy chain V r
33	61	63.5	106	2 S24256	Ig heavy chain V r
34	61	63.5	108	2 PH1648	Ig heavy chain V r
35	61	63.5	109	2 S24254	Ig heavy chain V r
36	61	63.5	109	2 S24253	Ig heavy chain V r
37	61	63.5	109	2 PH1649	Ig heavy chain V r
38	61	63.5	110	2 S24250	Ig heavy chain V r
39	61	63.5	112	2 PH1647	Ig heavy chain V r
40	61	63.5	113	2 S24247	Ig heavy chain - c
41	61	63.5	115	2 S09382	Ig heavy chain pre
42	61	63.5	117	2 A45953	Ig heavy chain - h
43	61	63.5	118	2 S31121	Ig heavy chain V r
44	61	63.5	119	2 D36005	Ig heavy chain - h
45	61	63.5	119	2 S31107	Ig heavy chain V r
46	61	63.5	119	2 C36005	Ig heavy chain - h
47	61	63.5	119	2 S31108	Ig heavy chain V r
48	61	63.5	120	2 S48798	Ig heavy chain - h
49	61	63.5	121	2 S31113	Ig heavy chain - h
50	61	63.5	121	2 I55673	Ig heavy chain - h
51	61	63.5	123	2 S31114	Ig heavy chain - h
52	61	63.5	127	2 S38489	Ig heavy chain V r
53	61	63.5	138	2 S31666	Ig heavy chain V r
54	61	63.5	140	2 S31586	Ig heavy chain var
55	61	63.5	145	2 I47203	Ig heavy chain var
56	61	63.5	148	2 I47210	Ig heavy chain var
57	61	63.5	160	2 S05271	Ig heavy chain pre
58	60	62.5	117	2 PH1552	Ig heavy chain V r
59	60	62.5	118	2 S00700	Ig heavy chain V-1
60	60	62.5	122	2 A33989	Ig heavy chain var
61	60	62.5	137	2 I47193	Ig heavy chain V r
62	59	61.5	98	2 S29545	Ig heavy chain V r
63	59	61.5	113	2 S02717	Ig heavy chain V r
64	59	61.5	115	2 PH1538	Ig heavy chain pre
65	59	61.5	117	1 HWSRF	Ig H chain V regio
66	59	61.5	119	2 PH1548	Ig H chain V regio
67	59	61.5	119	2 PH1549	Ig heavy chain V r
68	58	60.4	134	2 S31699	Ig heavy chain V r
69	58	60.4	140	2 S31686	Ig heavy chain var
70	58	60.4	143	2 I47202	Ig heavy chain V r
71	57	59.4	98	2 S26896	Ig heavy chain V r
72	57	59.4	98	2 S26933	Ig heavy chain pre
73	57	59.4	117	1 H3H026	Ig heavy chain V r
74	57	59.4	120	2 E49590	Ig heavy chain V r
75	56.5	58.9	97	2 S26885	Ig heavy chain V r
76	56.5	58.9	97	2 S26886	Ig heavy chain - h
77	56.5	58.9	116	2 S12557	Ig heavy chain V r
78	56	58.3	113	2 S25571	Ig heavy chain V r
79	55.5	57.8	86	2 S26788	Ig heavy chain V r
80	55	57.3	96	2 S54854	Ig heavy chain V r
81	55	57.3	117	2 PH1553	Ig H chain V regio
82	55	57.3	140	2 I47204	Ig heavy chain var
83	54.5	56.8	147	2 I47183	Ig heavy chain var
84	54.5	56.8	148	2 I47180	Ig heavy chain V r
85	54	56.2	111	2 S51211	Ig heavy chain V r
86	54	56.2	113	2 A34964	Ig heavy chain pre
87	54	56.2	124	2 S20782	Ig heavy chain V r
88	54	56.2	145	2 I47186	Ig heavy chain var
89	53.5	55.7	342	2 A46529	Ig gamma chain (5-
90	53	55.2	98	2 PL0121	Ig heavy chain V-I
91	53	55.2	108	2 PH1011	Ig heavy chain V r
92	53	55.2	111	2 S69911	Ig V-D-J region (R
93	53	55.2	115	1 A2H0BU	Ig V-D-J region (R
94	53	55.2	125	2 S72665	Ig heavy chain var
95	53	55.2	133	2 I47195	Ig heavy chain pre
96	53	55.2	137	2 S78054	Ig heavy chain V r
97	52.5	54.7	98	2 S26932	Ig heavy chain var
98	52	54.2	146	2 I47196	Ig heavy chain var
99	52	54.2	151	2 A60943	Ig heavy chain pre
100	52	54.2	151	2 A60943	Ig heavy chain pre


```

Best Local Similarity 76.5%; Pred.No. 0.00052;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKVG 17
DB 50 GITWNSGRIGYADSVKVG 66
||| | |||||
||| | |||||

RESULT 9
S26934
IG heavy chain V region (DP-59) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26934
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty gr
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26934
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TM>
A:Cross-references: UNIPARC:UPI0000116415; EMBL:Z12359; NID:G32937; PIDN:CAA782
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 98;
Best Local Similarity 70.6%; Pred.No. 0.001;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKVG 17
DB 50 GVSWNGSRTHYADSVKVG 66
||:|||| | |||||
||:|||| | |||||

RESULT 10
S26929
IG heavy chain V region (DP-33) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26929
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty gr
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26929
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TM>
A:Cross-references: UNIPARC:UPI000011640A; EMBL:Z12335; NID:G32889; PIDN:CAA782
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 98;
Best Local Similarity 81.2%; Pred.No. 0.001;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 INWNGSGTGYADSVKVG 17
DB 51 ISWDGGSTYYADSVKVG 66
||:|||| | |||||
||:|||| | |||||

RESULT 11
S44111
IG heavy chain V-D-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44111
R:Hawking, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.J.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of

```

A;Reference number: S44105

A;Accession: S44111

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-120 <HAW>

A;Cross-references: UNIPARC:UPI000011662E; EMBL:Z31387; NID:G472965; PIDN:CAA83262.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 120;

Best Local Similarity 81.2%; Pred. No. 0.0012;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 INWNGSGTGYADSVKG 17

Db 51 ISWDGGSTYYADSVKG 66

RESULT 12

JL0048

Ig heavy chain V region precursor (clone cR19) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 15-Mar-2004

C;Accession: JL0048; S66433

R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.

J. Exp. Med. 167, 2011-2016, 1988

A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new 5

A;Reference number: JL0047; MUID:88258392; PMID:3133445

A;Accession: JL0048

A;Molecule type: mRNA

A;Residues: 1-191 <BEA>

A;Cross-references: UNIPARC:UPI000017C256

A;Note: the authors translated the reading frame which extends to the stop codon; the se

R;Mueller-Newen, G.; Koelne, C.; Keul, R.; Hemmann, U.; Mueller-Esterl, W.; Wijdenes, J.

Eur. J. Biochem. 236, 837-842, 1996

A;Title: Purification and characterization of the soluble interleukin-6 receptor from hu

A;Reference number: S66433; MUID:96270733; PMID:8665902

A;Accession: S66433

A;Molecule type: protein

A;Residues: 9-18 <MUE>

A;Cross-references: UNIPARC:UPI000017C257

C;Keywords: heterotetramer; immunoglobulin

F;23-106/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 71; DB 2; Length 191;

Best Local Similarity 70.6%; Pred. No. 0.002;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17

Db 58 GVSWNGSRTHYADSVKG 74

RESULT 13

GIHUDB

Ig heavy chain V-III region (Dob) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence_revision 31-Dec-1979 #text_change 09-Jul-2004

C;Accession: A90431; A02065

R;Steiner, L.A.; Garcia Pardo, A.; Margolies, M.N.

Biochemistry 18, 4068-4080, 1979

A;Title: Amino acid sequence of the heavy-chain variable region of the crystallizable hu

A;Reference number: A90431; MUID:80020921; PMID:114209

A;Accession: A90431

A;Molecule type: protein

A;Residues: 1-120 <STE>

A;Cross-references: UNIPROT:P01782; UNIPARC:UPI000012CF05

R;Steiner, L.A.; Lopes, A.D.

Biochemistry 18, 4054-4067, 1979

A;Title: The crystallizable human myeloma protein Dob has a hinge-region deletion.

A;Reference number: A90430; MUID:80020920; PMID:114208

A;Contents: annotation

A;Note: this gamma-1 myeloma protein has a deletion in the hinge region; there are no li

C;Genetics:

A;Gene: GDB:IGHV@

A;Cross-references: GDB:128528; OMIM:147070

A;Map position: 14q32.33-14q32.33

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match 71.9%; Score 69; DB 1; Length 120;

Best Local Similarity 81.2%; Pred. No. 0.0025;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 INWNGSGTGYADSVKG 17

Db 51 ITWNGSVLYADSVKG 66

RESULT 14

S11239

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S11239

R;Felgenhauer, M.; Kohl, J.; Rueker, F.

Nucleic Acids Res. 18, 4927, 1990

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A;Reference number: S11239; MUID:90370490; PMID:1697678

A;Accession: S11239

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-145 <REL>

A;Cross-references: UNIPARC:UPI0000113781; EMBL:X53613; NID:G23865; PIDN:CAA37675.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 68; DB 2; Length 145;

Best Local Similarity 70.6%; Pred. No. 0.0043;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17

Db 69 GISWDSSSIGYADSVKG 85

RESULT 15

S36273

Ig heavy chain V region (clone alpha-THY-32) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C;Accession: S36273

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries.

A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: S36273

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-120 <GRI>

A;Cross-references: UNIPARC:UPI0000118DE4; EMBL:Z18834; NID:G33116; PIDN:CAA79286.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 65; DB 2; Length 120;

Best Local Similarity 76.5%; Pred. No. 0.01;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGYADSVKG 17

Db 1 GINWNGSGTGYADSVKG 17

Db 50 GISSNSGSGTYADSVK 66

RESULT 16

PC4281 anti-SS-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: PC4281
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltrating lymphocytes
A:Reference number: PC4279, MUID:97236289; PMID:9125110
A:Accession: PC4281

A:Molecule type: protein

A:Residues: 1-123 <SUZ>

A:CROSS-references: UNIPARC:UPI0000176E91

C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren's syndrome
C:Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

Query Match 67.7%; Score 65; DB 2; Length 123;

Best Local Similarity 68.8%; Pred. No. 0.01;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 INWNGSGTYADSVK 17

||| : ||| |||||

Db 51 ISWNSGTGYMDSVK 66

RESULT 17

S24248 Ig heavy chain V region (VH26) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S24248

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24248

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-90 <STE>

A:CROSS-references: UNIPARC:UPI000011608D; EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 66.7%; Score 64; DB 2; Length 90;

Best Local Similarity 76.5%; Pred. No. 0.011;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTYADSVK 17

||| : ||| |||||

Db 49 GISGSGSTTYADSVK 65

RESULT 18

S36278 Ig heavy chain V region (clone alpha-THY-23) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C:Accession: S36278

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries

A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36278

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-120 <GRI>

A:CROSS-references: UNIPARC:UPI0000118DE2; EMBL:Z18830; NID:g33114; PIDN:CAA79282.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin ;
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 64; DB 2; Length 120;

Best Local Similarity 76.5%; Pred. No. 0.014; 2; Indels 0; Gaps 0;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTYADSVK 17

||| : ||| |||||

Db 50 GISGSGSTTYADSVK 66

RESULT 19

S20781 Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20781

R:Mortari, F.; Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A:Description: Analysis of human cord blood Ig heavy chain IGA and IGG repertoire.

A:Reference number: S20764

A:Accession: S20781

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <MOR>

A:CROSS-references: UNIPARC:UPI00001163E9; EMBL:Z11945; NID:g33895; PIDN:CAA78002.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 64.6%; Score 62; DB 2; Length 96;

Best Local Similarity 56.5%; Pred. No. 0.023;

Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTYADSVK 17

| : | : ||| |||||

Db 19 GLEWVSATSVSGSTHYADSVK 41

RESULT 20

S26935 Ig heavy chain V region (DP-42) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26935

R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26935

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <TOM>

A:CROSS-references: UNIPARC:UPI000011640E; EMBL:Z12342; NID:g32905; PIDN:CAA78212.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 61.5; DB 2; Length 97;

Best Local Similarity 59.1%; Pred. No. 0.027; 2; Indels 5; Gaps 1;

Matches 13; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 1 GINW-----NGSGTYADSVK 17

| : | : ||| |||||

Db 44 GLEWVSIVYSGSTHYADSVK 65

RESULT 21

S46462 Ig heavy chain V region (YAC-5) - human

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S46462

R; Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Buluwela, L.; Wil
Nature Genet. 7, 162-168, 1994
A; Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A; Reference number: S46460; MUID:95004581; PMID:7920635
A; Accession: S46462
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-97 <COO>
A; Cross-references: UNIPARC:UPI00001165D9; EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PT
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotrimer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 61.5; DB 2; Length 97;
Best Local Similarity 59.1%; Pred. No. 0.027;
Matches 13; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17
| : | : ||| |||||
Db 44 GLEWVSVIYSGSTYYADSVKG 65

RESULT 22

Ig heavy chain precursor V-region chain 5A - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Aug-1996
C; Accession: B28966; A3782
R; Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 1566-1570, 1988
A; Title: Immunoglobulin heavy chain variable region gene evolution: structure and family
A; Reference number: A28966; MUID:88144476; PMID:3125551
A; Accession: B28966
A; Molecule type: DNA
A; Residues: 1-116 <WIL>
A; Cross-references: UNIPARC:UPI000013CEDE
R; Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 3276, 1989
A; Reference number: A32782
A; Contents: annotation; erratum
A; Note: the authors note that this sequence is of higher primate (probably human) origin
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotrimer; immunoglobulin
F; 34-116/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 61.5; DB 2; Length 116;
Best Local Similarity 59.1%; Pred. No. 0.033; 2; Indels 5; Gaps 1;
Matches 13; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKG 17
| : | : ||| |||||
Db 63 GLEWVSVIYSGSTYYADSVKG 84

RESULT 23

S31110
Ig heavy chain - human
C; Species: Homo sapiens (man)
C; Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C; Accession: S31110
R; Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar
Eur. J. Immunol. 22, 247-251, 1992
A; Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A; Reference number: S31104; MUID:92111633; PMID:1730252
A; Accession: S31110
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-116 <RAA>
A; Cross-references: UNIPARC:UPI0000176E36; EMBL:X62958
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotrimer; immunoglobulin
F; 15-97/Domain: immunoglobulin homology <IMM>

A:Reference number: S54856

A:Accession: S54856

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TM>

A:Cross-references: UNIPARC:UPI00001164A5; EMBL:Z18901; NID:G840778; PIDN:CAA79338.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 98;

Best Local Similarity 56.5%; Pred. No. 0.033;

Matches 13; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GINW-----NGSGTGADSVK 17

Db 44 GLEWVSLISGGSGSTYYADSVK 66

RESULT 27

IG heavy chain V region (VH26-DK1-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S24259

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24259

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99 <STE>

A:Cross-references: UNIPARC:UPI000011608B; EMBL:X67067; NID:G38391; PIDN:CAA47452.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-83/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 99;

Best Local Similarity 56.5%; Pred. No. 0.033;

Matches 13; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GINW-----NGSGTGADSVK 17

Db 29 GLEWVSAISGGSGSTYYADSVK 51

RESULT 28

IG heavy chain V region (VH26-DXP1-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S24258

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24258

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-100 <STE>

A:Cross-references: UNIPARC:UPI000011608A; EMBL:X67066; NID:G38389; PIDN:CAA47451.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-86/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 100;

Best Local Similarity 56.5%; Pred. No. 0.033;

Matches 13; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GINW-----NGSGTGADSVK 17

Db 32 GLEWVSAISGGSGSTYYADSVK 54

RESULT 29

S24257

IG heavy chain V region (VH26-DXP1-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S24257

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24257

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <STE>

A:Cross-references: UNIPARC:UPI0000116089; EMBL:X67065; NID:G38387; PIDN:CAA47450.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-93/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 101;

Best Local Similarity 56.5%; Pred. No. 0.034;

Matches 13; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GINW-----NGSGTGADSVK 17

Db 39 GLEWVSAISGGSGSTYYADSVK 61

RESULT 30

S24260

IG heavy chain V region (VH26-DAL-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004

C:Accession: S24260

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24260

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <STE>

A:Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176E5C; EMBL:X67068

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:5-87/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 102;

Best Local Similarity 56.5%; Pred. No. 0.034;

Matches 13; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 GINW-----NGSGTGADSVK 17

Db 33 GLEWVSAISGGSGSTYYADSVK 55

RESULT 31

S24255

IG heavy chain V region (VH26-DLR5-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S24255

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STE>

A:Cross-references: UNIPARC:UPI0000176E60; EMBL:X67063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

QY 1 GINW-----NGSGTGYADSVK 17
|:|:|||||
Db 40 GLEWVSAISGGSGTYYADSVK 62

RESULT 37

PH1649
IG heavy chain V region (clone 2B7) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1649
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcus aureus
A:Reference number: PH1642; PMID:93301610; PMID:8315388

A:Accession: PH1649

A:Molecule type: mRNA

A:Residues: 1-109 <HIL>

A:Cross-references: UNIPARC:UPI0000176BD6

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 109;

Best Local Similarity 56.5%; Pred. No. 0.037; 2; Indels 2; Gaps 1;

Matches 13; Conservative 2; Mismatches 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVK 17
|:|:|||||
Db 36 GLEWVSAISGGSGTYYADSVK 58

RESULT 38

S24250
IG heavy chain V region (VH26-DN1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24250
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247

A:Accession: S24250

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-110 <STE>

A:Cross-references: UNIPARC:UPI0000176D50; EMBL:X67071

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 110;

Best Local Similarity 56.5%; Pred. No. 0.037; 2; Indels 2; Gaps 1;

Matches 13; Conservative 2; Mismatches 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVK 17
|:|:|||||
Db 43 GLEWVSAISGGSGTYYADSVK 65

RESULT 39

PH1647
IG heavy chain V region (clone 2D10) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1647
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcus aureus
A:Reference number: PH1642; PMID:93301610; PMID:8315388

A:Accession: PH1647

A:Molecule type: mRNA
A:Residues: 1-112 <HIL>
A:Cross-references: UNIPARC:UPI0000176BD4
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 112;
Best Local Similarity 56.5%; Pred. No. 0.038;
Matches 13; Conservative 2; Mismatches 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVK 17
|:|:|||||
Db 36 GLEWVSAISGGSGTYYADSVK 58

RESULT 40

S24247
IG heavy chain V region (VH26-DLR2-JH3) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24247
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24247
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <STE>
A:Cross-references: UNIPARC:UPI0000116084; EMBL:X67060; NID:938377; PIDN:CAA47445.1; P11
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 61; DB 2; Length 113;
Best Local Similarity 56.5%; Pred. No. 0.038;
Matches 13; Conservative 2; Mismatches 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVK 17
|:|:|||||
Db 43 GLEWVSAISGGSGTYYADSVK 65

Search completed: November 18, 2005, 21:15:27
Job time : 38.2143 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 20:58:05 ; Search time 220.393 Seconds
(without alignments)
54.421 Million cell updates/sec

Title: US-10-029-926D-115

Perfect score: 96

Sequence: 1 GINWNGSGTGYADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	112	2	Q9HCC1_HUMAN
2	84	87.5	499	2	Q8NSK4_HUMAN
3	82	85.4	494	2	Q6ZM64_HUMAN
4	79	82.3	104	2	Q9UL87_HUMAN
5	79	82.3	573	2	Q8WU38_HUMAN
6	73	76.0	472	2	Q6N089_HUMAN
7	71	74.0	469	2	Q569F4_HUMAN
8	69	71.9	120	1	HV3U_HUMAN
9	61.5	64.1	116	1	HV05_CARAU
10	61	63.5	121	2	Q9UL71_HUMAN
11	61	63.5	593	2	Q6INN5_XENLA
12	61	63.5	597	2	Q96BB9_HUMAN
13	61	63.5	614	2	Q6DDQ7_XENLA
14	60	62.5	584	2	Q6INK3_XENLA
15	60	62.5	589	2	Q5XHD5_XENLA
16	59	61.5	117	1	HV53_MOUSE
17	59	61.5	493	2	Q6GMX2_HUMAN
18	58	60.4	367	2	Q5MBX4_XENTR
19	58	60.4	467	2	Q4VBH1_RAT
20	57	59.4	117	1	HV3C_HUMAN
21	56	58.3	118	2	Q9UL72_HUMAN
22	55	57.3	479	2	Q91WP5_MOUSE
23	54.5	56.8	96	2	Q4SX92_TETNG
24	54.5	56.8	466	2	Q6IN78_HUMAN
25	54	56.2	112	2	Q9UGP3_HUMAN
26	53	55.2	115	1	HV3P_HUMAN
27	52	54.2	470	2	Q68CN4_HUMAN
28	52	54.2	591	2	Q5I0L9_RAT
29	51	53.1	121	1	HV3J_HUMAN
30	51	53.1	469	2	Q9FDT2_9GAMM
31	51	53.1	475	2	Q6MZQ6_HUMAN

32	51	53.1	479	2	Q5PQK9_RAT	Q5PQK9 rattus norv
33	51	53.1	838	1	Q7UUV9_RHOBA	Q7UUV9 rhodopirell
34	50.5	52.6	97	1	HV56_MOUSE	P18527 mus musculu
35	50	52.1	874	2	Q6C6K4_YARLI	Q6C6K4 yarrowia li
36	49	51.0	767	2	Q9U234_CAEEL	Q9U234 caenorhabdi
37	49	51.0	1089	2	Q5LD46_BACFN	Q5LD46 bacteroides
38	49	51.0	1089	2	Q64U63_BACFR	Q64U63 bacteroides
39	48.5	50.5	117	1	HV02_CANFA	P01785 canis famli
40	48	50.0	99	2	Q6B743_RABIT	P18526 mus musculu
41	48	50.0	117	1	HV55_MOUSE	Q6B743 oryctolagus
42	48	50.0	119	1	HV3L_HUMAN	P01773 homo sapien
43	48	50.0	258	2	Q5BAC0_EMENI	O5BAC0 aspergillus
44	48	50.0	279	2	Q9WZJ8_THEMA	Q9WZJ8 thermotoga
45	48	50.0	298	2	Q9XGB4_TRIRP	Q9XGB4 trifolium r
46	48	50.0	320	2	Q4W1D2_9XANT	Q4W1D2 xanthomonas
47	48	50.0	416	2	Q9NPP6_HUMAN	Q9NPP6 homo sapien
48	48	50.0	458	2	Q5M842_RAT	Q5M842 rattus norv
49	48	50.0	469	2	Q4V092_XANCP	Q4V092 xanthomonas
50	48	50.0	469	2	Q8PDZ8_XANCP	Q8PDZ8 xanthomonas
51	48	50.0	473	2	Q91Z05_MOUSE	Q91Z05 mus musculu
52	48	50.0	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
53	48	50.0	654	2	Q86AX3_DICDI	Q86AX3 dictyosteli
54	48	50.0	713	2	Q4IA18_GIBZE	Q4IA18 gibberella
55	48	50.0	757	2	Q60YWS_CAEER	Q60YWS caenorhabdi
56	48	50.0	761	2	Q20898_CAEEL	Q20898 caenorhabdi
57	48	50.0	4342	2	Q91157_PSEAE	Q91157 pseudomonas
58	47.5	49.5	100	2	Q6B755_RABIT	Q6B755 oryctolagus
59	47.5	49.5	739	2	Q5M1S2_STRT1	Q5M1S2 streptococc
60	47	49.0	87	2	Q7Y3K4_9CAUD	Q7Y3K4 enterobacte
61	47	49.0	116	2	Q9UL93_HUMAN	Q9UL93 homo sapien
62	47	49.0	117	1	HV54_MOUSE	P18525 mus musculu
63	47	49.0	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
64	47	49.0	469	2	Q87CN9_XYLFT	Q87CN9 xylella fas
65	47	49.0	515	2	Q16968_APLCA	Q16968 aplysia cal
66	47	49.0	519	2	Q6N092_HUMAN	Q6N092 homo sapien
67	47	49.0	613	2	Q8WUK1_HUMAN	Q8WUK1 homo sapien
68	47	49.0	1144	2	Q57ZN3_9TRYP	Q57ZN3 trypanosoma
69	46.5	48.4	96	2	Q4SZG1_TETNG	Q4SZG1 tetraodon n
70	46.5	48.4	99	2	Q4T5M5_TETNG	Q4T5M5 tetraodon n
71	46.5	48.4	135	1	HV02_XENLA	P20957 xenopus lae
72	46	47.9	113	2	Q9UL50_HUMAN	Q9UL50 homo sapien
73	46	47.9	114	1	HV3B_HUMAN	P01763 homo sapien
74	46	47.9	115	1	HV3D_HUMAN	P01765 mus musculu
75	46	47.9	117	1	HV03_CARAU	P19180 carassius a
76	46	47.9	119	1	HV3M_HUMAN	P01774 homo sapien
77	46	47.9	122	1	HV3A_HUMAN	P01775 homo sapien
78	46	47.9	122	1	HV3A_HUMAN	P01762 homo sapien
79	46	47.9	126	2	Q9UL84_HUMAN	Q9UL84 homo sapien
80	46	47.9	131	2	HV3K_HUMAN	Q9UL88 homo sapien
81	46	47.9	159	2	Q720U0_LISMP	Q720U0 listeria mo
82	46	47.9	159	2	Q8Y7X8_LISMP	Q8Y7X8 listeria mo
83	46	47.9	159	2	Q92CR6_LISIN	Q92CR6 listeria in
84	46	47.9	260	2	Q8NPS3_CONGL	Q8NPS3 corynebacte
85	46	47.9	407	2	Q5TSR0_ANOGA	Q5TSR0 anopheles g
86	46	47.9	410	2	Q5RM08_MOUSE	Q5RM08 mus musculu
87	46	47.9	410	2	Q6IMK1_RAT	Q6IMK1 rattus norv
88	46	47.9	413	2	Q7Z718_HUMAN	Q7Z718 homo sapien
89	46	47.9	414	2	Q5TSR1_ANOGA	Q5TSR1 anopheles g
90	46	47.9	428	1	SP7_MOUSE	Q8V167 mus musculu
91	46	47.9	428	1	Q6IMK2_RAT	Q6IMK2 rattus norv
92	46	47.9	431	1	SP7_HUMAN	Q811U1 rattus norv
93	46	47.9	431	1	SP7_HUMAN	Q811U1 rattus norv
94	46	47.9	464	2	Q8S7G0_ORISA	Q8S7G0 oryza sativ
95	46	47.9	465	2	Q5I0J0_RAT	Q5I0J0 rattus norv
96	46	47.9	466	2	Q7Q9J6_ANOGA	Q7Q9J6 anopheles g
97	46	47.9	469	2	Q5GU81_XANAC	Q5GU81 xanthomonas
98	46	47.9	469	2	Q8PQW5_XANAC	Q8PQW5 xanthomonas
99	46	47.9	473	2	Q9RBK1_XANCI	Q9RBK1 xanthomonas
100	46	47.9	473	2	Q9RBK1_XANCI	Q9RBK1 xanthomonas

ALIGNMENTS

```
RESULT 1
Q9HCC1_HUMAN
ID Q9HCC1_HUMAN PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -; mRNA.
DR HSP; P01783; IIGC.
DR SMR; Q9HCC1; 1-112.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 100.0%; Score 96; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GINWNGSTGYADSVK 17
DB 50 GINWNGSTGYADSVK 66

RESULT 2
Q9NSK4_HUMAN
ID Q9NSK4_HUMAN PRELIMINARY; PRT; 499 AA.
AC Q9NSK4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MG27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -; mRNA.
DR HSP; P01876; IOWO.
DR SMR; Q9NSK4; 269-477.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 499 AA; 53376 MW; 93A5C958582054F32 CRC64;

Query Match 87.5%; Score 84; DB 2; Length 499;
Best Local Similarity 93.8%; Pred. No. 0.00017;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 INWNGSTGYADSVK 17
DB 70 INWNGSTGYADSVK 85

RESULT 3
Q6ZW64_HUMAN PRELIMINARY; PRT; 494 AA.
ID Q6ZW64_HUMAN PRELIMINARY;
AC Q6ZW64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ41552.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Colon;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Megatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK123546; BAC85641.1; -; mRNA.
DR HSP; P01842; IAOK.
DR SMR; Q6ZW64; 264-472.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IGV; 4.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 494 AA; 53321 MW; CD8140B37A23A882 CRC64;
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Query Match      85.4%; Score 82; DB 2; Length 494;
Best Local Similarity 82.4%; Pred. No. 0.00034;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
Db 69 GIDWNGGDAGYADSVKG 85

RESULT 4
Q9UL87 HUMAN
ID Q9UL87_HUMAN PRELIMINARY; PRT; 104 AA.
AC Q9UL87
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.B., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035027; AAD56263.1; -; mRNA.
DR HSP; P01810; 2FBJ.
DR SMR; Q9UL87; 1-104.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 104
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40B9E67B CRC64;

Query Match      82.3%; Score 79; DB 2; Length 104;
Best Local Similarity 82.4%; Pred. No. 0.00019;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
Db 29 GISWNGSGIGYADSVKG 45

RESULT 5
Q8WU38 HUMAN
ID Q8WU38_HUMAN PRELIMINARY; PRT; 573 AA.
AC Q8WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH domain protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345 (1992).
DR EMBL; BC021276; AAH21276.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSP; P18529; I18K.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

Query Match      82.3%; Score 79; DB 2; Length 573;
Best Local Similarity 82.4%; Pred. No. 0.0012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVKG 17
Db 69 GISWNGSGIGYADSVKG 85

RESULT 6
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686P15220.
GN Name=DKF2p686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Rectum tumor;
RC The German cDNA Consortium;

```


RESULT 9
 HV05_CARAU STANDARD; PRT; 116 AA.
 ID HV05_CARAU STANDARD; PRT; 116 AA.
 AC P19181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Warr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 and family relationships of two genes and a pseudogene in a teleost
 fish."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 DR HSP; P01783; IIGC.
 DR SMR; P19181; 20-116.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 116 Ig heavy chain V region 5A.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 84 Complementarity-determining-2.
 FT REGION 85 116 Framework-3.
 FT DISULFID 41 114 By similarity.
 FT NON_TER 116 116
 FT SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;
 Query Match 64.1%; Score 61.5; DB 1; Length 116;
 Best Local Similarity 59.1%; Pred. No. 0.12;
 Matches 13; Conservative 2; Mismatches 5; Gaps 1;
 QY 1 GINW-----NGSGTGYADSVKG 17
 DB 63 GLEWVSVIYSGGTYADSVKG 84
 RESULT 10
 Q9UL71 HUMAN
 ID Q9UL71 HUMAN PRELIMINARY; PRT; 121 AA.
 AC Q9UL71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035043; AAD56279.1; -; mRNA.
 DR HSSP; P01852; INPD.
 DR SMR; Q9UL71; 1-121.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 121
 FT NON_TER 121 121
 FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;
 Query Match 63.5%; Score 61; DB 2; Length 121;
 Best Local Similarity 56.5%; Pred. No. 0.16;
 Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
 QY 1 GINW-----NGSGTGYADSVKG 17
 DB 44 GLEWVSLISGGGTYADSVKG 66
 RESULT 11
 Q6INM5 XENLA
 ID Q6INM5 XENLA PRELIMINARY; PRT; 593 AA.
 AC Q6INM5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC69066 protein.
 GN Name=MGC69066;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splice;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Schenck P., Prange C.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Mullaly S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splice;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RL NIH MGC Project;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072253; AAH72253.1; -, mRNA.
DR HS99; P01842; IADQ.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via ...; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.C1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR InterPro; IPR001680; WD40.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS0290; IG.MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS.1; UNKNOWN 1.
SQ SEQUENCE 593 AA; 65875 MW; B3314FF9311E12FC CRC64;

Query Match 63.5%; Score 61; DB 2; Length 593;
Best Local Similarity 81.2%; Pred. No. 0.83;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 INWGGSTGYADSVKVG 17
DB 68 INPDGGSTGYADSVKVG 83

RESULT 12
Q96BB9 HUMAN
ID Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S., Krzywinski M.I., Skalska U., Smalley D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Primary B-Cells;
NIH MGC Project;
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[3]
NUCLEOTIDE SEQUENCE.
PubMed=2500644;
Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
"Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
chains of a human monoclonal antibody with broad reactivity to
malignant tumor cells.";
Nucleic Acids Res. 17:4385-0 (1989).
EMBL; BC015760; AAH15760.1; -, mRNA.
PIR; S05271; S05271.
PIR; S24260; S24260.
HSSP; P01861; IADQ.
Ensembl; ENSG00000130076; Homo sapiens.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG.C1.
InterPro; IPR003006; IG.MHC.
InterPro; IPR003596; IG.V.
Pfam; PF07654; C1-set; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG LIKE; 5.
PROSITE; PS0290; IG.MHC; UNKNOWN 3.
KW Immunoglobulin domain.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 597;
Best Local Similarity 56.5%; Pred. No. 0.84;
Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGYADSVKVG 17
DB 63 GLEWVSAISGGSGTGYADSVKVG 85

RESULT 13
Q6DDQ7 XENLA
ID Q6DDQ7 XENLA PRELIMINARY; PRT; 614 AA.
AC Q6DDQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC69066 protein.
GN Name=MGC69066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```


Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Splice;
RC Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077477.1; -, mRNA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . ; IEA.
DR DR InterPro; IPR003599; Ig.
DR DR InterPro; IPR007110; Ig-Like.
DR DR InterPro; IPR003597; Ig cl.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR InterPro; IPR003596; Ig_v.
DR DR InterPro; IPR001680; WD40.
DR DR Pfam; PF07654; Cl-set; 4.
DR DR SMART; SM00409; IG; 4.
DR DR SMART; SM00407; IGcl; 4.
DR DR SMART; SM00406; IGV; 1.
DR DR PROSITE; PSS00835; IG_LIKE; 5.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN 4.
DR DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
DR SQ SEQUENCE 614 AA; 69254 MW; 2631B7CF955270C0 CRC64;

Query Match 63.5%; Score 61; DB 2; Length 614;
Best Local Similarity 56.5%; Pred. No. 0.86; 2; Indels 6; Gaps
Matches 13; Conservative

QY 1 GINW-----NGGSGTYADSVKG 17
| : | : |||||
DB 61 GLQWVSIVSDGGSTYYADSVKG 83

RESULT 14
ID Q6INK3_XENLA PRELIMINARY; PRT; 584 AA.
AC Q6INK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OX xenopodinae; Xenopus; Xenopus.
NCBI TaxID=8355;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Lung;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klatschnig R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA FAhey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.B., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

(2)

NR NUCLEOTIDE SEQUENCE.

RC TISSUE=lung;

RX MEDLINE=223411132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative."; Dev. Dyn. 225:384-391(2002).

RL

RN NUCLEOTIDE SEQUENCE.

RA Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. ENBL; BC072277; AAH72277.1; -; mRNA.

DR HSP: P01842; 1AOK.

GO: GO:0016021, C:integral to membrane; IEA.

DR InterPro: IPR003599; IG-

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003597; IG.cl.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF07654; CL-set; 3.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00409; IG; 4.

DR SMART: SM00407; IGC1; 4.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 5.

DR PROSITE: PS00230; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.

SQ SEQUENCE 584 AA; 64449 MW; F134A9DD169FID64 CRC64;

Quality Match 62.5%; Score 60; DB 2; Length 584;
Best Local Similarity 56.5%; Pred. No. 1.2;
Matches 13; Conservative 1; Mismatches 3; Indels 6; Gaps

Oy 1 GINW-----NGSGTGYADSVKG 17
| : | |||||
Db 63 GLQWVSRIISDGGSTVYADSVKG 85

RESULT 15

OS XHXDS XENLA

ID OSXHD5 XENLA PRELIMINARY; PRY; 589 AA.

AC OSXHD5;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;

RP [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSU=Whole;

RX MEDLINE=223411132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative."; Dev. Dyn. 225:384-391(2002).

RL

RN NUCLEOTIDE SEQUENCE.

RA Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases. ENBL; BC072277; AAH72277.1; -; mRNA.

DR HSP: P01842; 1AOK.

GO: GO:0016021, C:integral to membrane; IEA.

DR InterPro: IPR003599; IG-

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003597; IG.cl.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_v.

DR Pfam: PF07654; CL-set; 3.

DR Pfam: PF00047; IG; 1.

DR SMART: SM00409; IG; 4.

DR SMART: SM00407; IGC1; 4.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 5.

DR PROSITE: PS00230; IG_MHC; UNKNOWN_3.

KW Hypothetical protein.

SQ SEQUENCE 584 AA; 64449 MW; F134A9DD169FID64 CRC64;

Quality Match 62.5%; Score 60; DB 2; Length 584;
Best Local Similarity 56.5%; Pred. No. 1.2;
Matches 13; Conservative 1; Mismatches 3; Indels 6; Gaps

Oy 1 GINW-----NGSGTGYADSVKG 17
| : | |||||
Db 63 GLQWVSRIISDGGSTVYADSVKG 85

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RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Gerhardt D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084123; AAB84123.1; -; mRNA.
DR GO; GO:0030106; P: MHC class I receptor activity; IEA.
DR GO; GO:0019883; P: antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P: antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_4.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 589 AA; 65361 MW; DIA212699D569FCE CRC64;

Query Match 62.5%; Score 60; DB 2; Length 589;
Best Local Similarity 56.5%; Pred. No. 1.2;
Matches 13; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

Qy 1 GINW-----NGSGTGYADSVKG 17
Db 61 GLQVSAISDGGSGTYADSVKG 83

RESULT 16
HV53 MOUSE
ID HV53 MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16; Created)
DT 01-NOV-1990 (Rel. 16; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Ig heavy chain V region RF precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA LeVey N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
```

```
RL J. Exp. Med. 169:2007-2019 (1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; J0503; HVMSRF.
DR HSSP; P18529; 118K.
DR SMR; P18524; 20-117.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region RF.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 61.5%; Score 59; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.31;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 INNWGSGTGYADSVKG 17
Db 70 INSGSGTGYADSVKG 85

RESULT 17
O6GMX2 HUMAN
ID O6GMX2 HUMAN PRELIMINARY; PRT; 493 AA.
AC O6GMX2;
DT 05-JUL-2004 (TrEMBLrel. 27; Created)
DT 05-JUL-2004 (TrEMBLrel. 27; Last sequence update)
DE IGH1 protein.
DE IGH1 protein.
GN Name=IGH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

DR	EMBL; J00387793; AAH87793.1; -; mRNA.
DR	GO; GO:0030106; P:MHC class II receptor activity; IEA.
DR	GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR	GO; GO:0019888; P:antigen processing, endogenous antigen via . . .; IEA.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003597; IG cl.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF07654; Cl-set; 2.
DR	SMART; SM00409; IG; 3.
DR	SMART; SM00407; IGcl; 2.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR	Hypothetical protein.
DR	SEQUENCE 367 AA; 40058 MW; 66DE2E25CDF0CB34 CRC64;

```

Query Match          60.4%;   Score 58;   DB 2;   Length 367;
Best Local Similarity 52.2%;   Pred. No. 1.5;
Matches 12; Conservative 3; Mismatches 2; Indels
1 GIWV-----NGGTCGYADSVRG 17
| : ||| |||||
63 GLOWVSYISDGGSTYYADSVRG 85

```

RESULT 19
ID Q4VBH1 RAT PRELIMINARY; PRT; 467 AA.
AC Q4VBH1;
CD 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE LOC293354 protein.
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Rattus.
OX NCBI_Taxid=10116;
ON [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=i10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapeltono M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki B., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shveychenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH WGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

DR EMBL; BC095846; AAH95846.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 467 AA; 51651 MW; 1PF0328F50160ED3 CRC64;

Query Match 60.4%; Score 58; DB 2; Length 467;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 2 INWNGSGTGYADSVKG 17
Db 70 INTDGGSTYDPDSVKG 85

RESULT 20
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE IG heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81101090; PubMed=6450418;
RA Mathysesena G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 20-117.
RX MEDLINE=93209281; PubMed=7681398;
RA Mariette X., Tsapis A., Brouet J.C.;
RT "Nucleotide sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated glycoprotein."
RL Eur. J. Immunol. 23:846-851(1993).
RN [3]
RP 3D-STRUCTURE MODELING OF 20-117.
RX MEDLINE=86094276; PubMed=3866244;
RA Toyonaga B., Yoshikai Y., Vadasz V., Chin B., Mak T.W.;
RT "Organization and sequences of the diversity, joining, and constant region genes of the human T-cell receptor beta chain."
RL Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; J00236; AAA53516.1; -; Unassigned DNA.
DR EMBL; M35415; AAA58735.1; -; Genomic DNA.
DR PIR; A02047; H3HU26.
DR PDB; 1HOU; Model; H=20-117.
DR HGNC; HGNC:5545; IGHV0.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V-III region VH26.
FT DOMAIN 20 >117 IG-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
Query Match 59.4%; Score 57; DB 1; Length 117;
Best Local Similarity 52.2%; Pred. No. 0.64;
Matches 12; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
Qy 1 GINW-----NGSGTGYADSVKG 17
Db 63 GLEWVSAISGGSGSYGYDSVKG 85

RESULT 21
Q9UL72_HUMAN
ID Q9UL72_HUMAN PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Strigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion."
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; AF035042; AAD56278.1; -; mRNA.
DR PIR; S21205; S21205.
DR HSSP; P01783; IIGC.
DR SMR; Q9UL72; 1-118.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1 118
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
Query Match 58.3%; Score 56; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 INWNGSGTGYADSVKG 17
Db 50 VTYSGSGSYADSVKG 65
RESULT 22
Q91WP5_MOUSE
ID Q91WP5_MOUSE PRELIMINARY; PRT; 479 AA.

AC Q91WP5; ORFNames=GSTENG00011060001;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Igh-VJ558 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marta M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013656; AAH13656.1; -; mRNA.
 DR HSSP; P01789; 1MCP.
 DR SMR; Q91WP5; 20-236.
 DR Ensembl; ENSMUSG0000021155; Mus musculus.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003196; Ig_v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 479 AA; 51604 MW; ECB2D087748584F CRC64;
 Query Match 57.3%; Score 55; DB 2; Length 479;
 Best Local Similarity 62.5%; Pred. No. 5.9;
 Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 2 INWNGSTGYADSVK 17
 DB 70 INSNNGNTYYSDTWKG 85
 |||||:|||||
 RESULT 23
 Q4SX92 TESTNG
 ID Q4SX92_TESTNG PRELIMINARY; PRT; 96 AA.
 AC Q4SX92;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF12787, whole genome shotgun sequence.
 DE (Fragment).

GN ORFNames=GSTENG00011060001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Da Silva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CAAE01012787; CAF94740.1; -; Genomic_DNA.
 DR NON_TER 1 1
 FT NON_TER 96 96
 SQ SEQUENCE 96 AA; 10590 MW; 85BED88AAEE7486 CRC64;
 Query Match 56.8%; Score 54.5; DB 2; Length 96;
 Best Local Similarity 50.0%; Pred. No. 1.3;
 Matches 11; Conservative 4; Mismatches 2; Indels 5; Gaps 1;
 QY 1 GINW-----NGSGTGYADSVK 17
 DB 41 GLEWISAISGGSTYYSVK 62
 ||:|||||:|||||
 RESULT 24
 Q6IN78 HUMAN
 ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
 AC Q6IN78;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettenan M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH WGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSPB, P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam, PF07654; C1-set; 3.
DR SMART, SM00409; IG; 2.
DR SMART, SM00407; IGc1; 3.
DR SMART, SM00406; IGv; 1.
DR PROSITE, PS50835; IG LIKE; 4.
DR PROSITE, PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCDE81076E CRC64;

Query Match 56.8%; Score 54.5; DB 2; Length 466;
Best Local Similarity 54.5%; Pred. NO. 6.8;
Matches 12; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

Qy 1 GINW-----NGGSTGYADSVKG 17
| : | | | | |
Dd 63 GLEWVSVLYIGGATYYADSVKG 84

```

RESULT 25
Q9UGP3 HUMAN
ID Q9UGP3_HUMAN PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN Name-IgH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RA	Zafiroopoulos A., Kandilogianaki M., Dahlenborg C., Borrebaeck C.A.K.,	
RA	Kramovidis E.,	
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.	
DR	EMBL; AJ132560; CAB65078.1; -, mRNA.	
DR	HGSP; P01783; IIGC.	
DR	SMR; Q9UGP3; 1-105.	
DR	Ensembl; ENSG00000188443; Homo sapiens.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	SMART; SM00406; IGV; 1..	
DR	PROSITE; PSS0835; IG-Like; 1.	
FT	NON TER	1
FT	NON TER	112
FT	NON TER	112
SQ	SEQUENCE	112 AA; 12226 MW; 0A1F7082C7A8CE3 CRC64;

Query Match 56.2%; Score 54; DB 2; Length 112;
Best Local Similarity 69.8%; Pred. NO. 1.8;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 INWNGGSTGYADSVKG 17
||| : |||||
pb 34 INATSGTTDYADSVKG 49

RESULT 26

HV3F_HUMAN			
ID	PV3F_HUMAN	STANDARD;	PRT; 115 AA.
AC	P01767;		
DT	21-JUL-1986	(Rel. 01,	Created)
DI	21-JUL-1986	(Rel. 01,	Last sequence update)
DE	10-MAY-2005	(Rel. 47,	Last annotation update)
DG	Ig heavy chain V-III	region BUT.	
OS	Homo sapiens	(Human).	
OC	Eukaryota;	Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia;	Eutheria;	Euarctontoglires; Primates; Catarrhini; Hominidae;
OX	HOMO.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	PROTEIN SEQUENCE.		
RX	MEDLINE=78137069;	PubMed=416441;	
RA	Torano A., Putnam F.W.;		
RT	"Complete amino acid sequence of the alpha 2 heavy chain of a human IgA2 immunoglobulin of the A2m (2) allotype."		
RL	Proc. Natl. Acad. Sci. U.S.A.	75:966-969(1978).	
CC	-I-	MISCELLANEOUS:	The sequence of the alpha-2, A2m(2) allotype, C region of this myeloma protein is also given.
CC	-I-	SIMILARITY:	Contains 1 Ig-like (immunoglobulin-like) domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

CC -----
DR PIR; A02050; AZHUBU.
DR DR HSPP; P01783; 1IGC.
DR DR SMR; P01767; 1-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR DR InterPro; IPR007110; Ig-like.
DR DR InterPro; IPR003596; Ig_v.
DR DR SMART; SMO0406; IGV; 1.
DR DR PROSITE; PS50835; IG_LIKE; 1.
DR DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 123379 MW; 208876A7DF52DCF4 CRC64;

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Query Match	55.2%	Score 53;	'DB 1;	Length 115;
Best Local Similarity	71.4%	Pred. No. 2.7;		

Qy 4 WNGSGTGYADSVKG 17
: ||: |||||
Dp 52 YRGGTTYADSVKG 65

RESULT 27

Q680M1_HUMAN
Q68CN4_HUMAN PRELIMINARY; PRT; 470 AA.
ID Q68CN4_HUMAN PRELIMINARY;
AC Q68CN4;
DT 23-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFzp686E23209.
DE Name=DKFzp686E23209;
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

```
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.2; -; mRNA.
DR SMR; Q68CN4; 43-493.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51536 MW; 7CB061DFC03D0B2B CRC64;

Query Match 54.2%; Score 52; DB 2; Length 470;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 INWNGSGTGADSVK 17
DB 70 ISYGGKQHYADSVK 85

RESULT 28
Q510L9 RAT PRELIMINARY; PRT; 591 AA.
AC Q510L9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC366747 protein (Fragment).
GN Names=LOC366747;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakeley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalka U., Smalhus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
```

```

RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC088184; AAH88184.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
FT NON TER 1
SQ SEQUENCE 591 AA; 64940 MW; 207CFE500D2C2A97 CRC64;

Query Match 54.2%; Score 52; DB 2; Length 591;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 GINWNGSGTGADSVK 16
DB 69 GWNWGGGTAYNSALK 84

RESULT 29
HV3J HUMAN STANDARD; PRT; 121 AA.
AC HV3J_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
cryoimmunoglobulin IGG Hil.";
RL Biochemistry 18:553-560 (1979).
CC -!- MISCELLANEOUS: This chain was isolated from an Igg1 myeloma
protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02054; GIHULH.
CC HSSP; P01772; 2FB4.
CC SMR; P01771; 2-121.
CC GO; GO:0005576; C: extracellular region; NAS.
CC GO; GO:0003823; F: antigen binding; NAS.
CC GO; GO:0006955; P: immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
```

FT	DOMAIN	1	112	Ig-like.
FT	MOD_RES	1	1	Pyroolidone carboxylic acid.
FT	NON_TER	121	121	
SQ	SEQUENCE	121 AA;	13566 MW;	480FC53610BF5DAB CRC64;

Query Match	53.1%	Score 51	DB 1	Length 121
Best Local Similarity	47.8%	Pred. No. 5.8		
Matches 11	Conservative	1	Mismatches	5
			Indels	6
			Gaps	1

Qy 1 GINW-----NGGSTGYADSVKG 17
| : | | | |
Dd 44 GLEWVAVIWYNGSRITYGDSVKG 66

RESULT 30	
Q9FDT2_9GAMM	
ID	Q9FDT2_9GAMM PRELIMINARY;
AC	Q9FDT2;
DT	01-MAR-2001 (TREMBlrel. 16, Created)
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE	DE Glutamine synthetase.
GN	Name=glNA;
OS	Shewanella benthica.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC	Shewanellaceae; Shewanella.
OX	NCBI TaxID=43661;

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DB6705;
RA Kato C.;
RL Submitted (F88-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB038330; BAB11930.1; -; Genomic_DNA.
DR HSSP; P06201; 1LGR.

DR GO:GO:0005377; C:cytoplasm; IEA.
DR GO:GO:0004356; F:glutamate-ammonia ligase activity; IEA.
DR GO:GO:016874; F:ligase activity; IEA.
DR GO:GO:0006542; P:glutamine biosynthesis; IEA.
DR GO:GO:0009399; P:nitrogen fixation; IEA.

```
DR InterPro; IPR004809; GlnA.  
DR InterPro; IPR001637; GlnA_adenyltn_S.  
DR InterPro; IPR008147; Gln_synt_beta.  
DR InterPro; IPR008146; Gln_synt_C.
```

DR PFam; PF00120; Gln-synt_C; 1.
DR PFam; PF03951; Gln-synt_N; 1.
DR ProDom; PD001057; Gln-synt_C; 1.
DR TIGRFAMs; TIGR00653; GlnA; 1.

DR PROSITE; PS00180; GLNA_1; 1.
DR PROSITE; PS00182; GLNA_ADENYLATION; 1.
DR PROSITE; PS00181; GLNA_ATP; 1.
KW Ligase.

SQ	SEQUENCE	469 AA; 51791 MW; 8FDA038A6EAAC14A CRC64;
Query Match	53.1%	Score 51; DB 2; Length
Best Local Alignment	52.0%	Score 49; DB 2; Length

	Matches	9;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	GINWNGSGTGYADSVKG	17							

RESULT 31
Q6MZQ6 HUMAN
ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475

AC	05-JUL-2004	(TRENBLrel. 27, Created)
DT	05-JUL-2004	(TRENBLrel. 27, Last sequence update)
DT	05-JUL-2004	(TRENBLrel. 27, Last annotation update)
DE	Hypothetical protein DKFZp686G1190.	

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC
OC
CN NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Newes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RA Submitted (JAN-2005) to the EMBL/GenBank/DBJP databases.
RL EMBL: BX640947; CAE45972.1; -: mRNA.

DR SMK; Q6MZQ6; 20-473.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.

DR DR InterPro; IPR003006; IG_MHC.
DR DR InterPro; IPR003596; IG_v.
DR DR Pfam; PF07654; C1-set; 3.
DR DR SMART; SM00409; IG_2.

DR SMART; SM00407; IGCI; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC. UNKNOWN 2

KW Hypothetical protein. B7EAE255A26F4B8E CRC64:
SO SEQUENCE 475 AA: 52043 MW:

Query Match 53.1%; Score 51; DB 2; Length 475;
Best Local Similarity 64.7%; Pred. No. 25;
Matches 11; Conservative 3; Mismatches 3; Indels

Qy 1 GINWGGSTGYADSVKG 17
||:|:|:|:|
Db 69 GISSSGWNTYYADSVKG 85

RESULT 32

Q3PQK9 RAT PRELIMINARY; 479 AA.
ID Q5PQK9 RAT PRELIMINARY; PRT;

DT	01-FEB-2005	(TREMBLrel. 29, Created)
DT	01-FEB-2005	(TREMBLrel. 29, Last sequence update)
DT	01-FEB-2005	(TREMBLrel. 29, Last annotation update)

GN Name=Igha;

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.

```
OK NCBI_taxid=10110,  
RN [1]
```

RC TISSUE=Lung;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wegner L., Shennen C.W., Schuler G.D.,
RA Altschul S.F., Zengerg B., Suecaw K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human


```
RT and mouse cDNA sequences.":
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087137; AAH87137.1; -, mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3..
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;

Query Match 53.1%; Score 51; DB 2; Length 479;
Best Local Similarity 47.8%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 5; Indels 6; Gaps 1;

QY 1 GINW-----NGSGTGADSVKG 17
DB 63 GLEWVASITNTGGKTYPDVSKG 85

RESULT 33
QYUUV9_RHOBA
ID QYUUV9_RHOBA PRELIMINARY; PRT; 838 AA.
AC QYUUV9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB3034;
OS Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner P.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294138; CAD72968.1; -, Genomic_DNA.
DR InterPro; IPR011478; DUF1585.
DR InterPro; IPR011429; PSC3.
DR Pfam; PF07635; PSCyt1; 1.
DR Pfam; PF07627; PSCyt3; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 838 AA; 91417 MW; 3321CFA9EA0336 CRC64;

Query Match 53.1%; Score 51; DB 2; Length 838;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 INWNGSGTGADSVK 16
DB 218 IKWGGTVAYATSVK 232

RESULT 34
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; J70504; HVMS91.
DR HSSP; P01783; IIGC.
DR SMR; P18527; 1-97.
DR Ensembl; ENSMUSG0000062386; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG.v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region.
FT DOMAIN 1 >97
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 52.6%; Score 50.5; DB 1; Length 97;
Best Local Similarity 52.4%; Pred. No. 5;
Matches 11; Conservative 2; Mismatches 3; Indels 5; Gaps 1;

QY 2 INW-----NGSGTGADSVKG 17
DB 45 LEWVASISSGGSTYYPDSVKG 65

RESULT 35
Q6C6K4_YARLI
ID Q6C6K4_YARLI PRELIMINARY; PRT; 874 AA.
AC Q6C6K4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to wi|NCU04755.1 Neurospora crassa NCU04755.1 hypothetical
DE protein (Fragment).
GN OrderedLocusNames=YALI0E08866g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
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RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lessur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Weslowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
EL Nature 430:35-44(2004);
DR EMBL; CR382131; CAG79297.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW Complete proteome; Hypothetical protein.
FT NOW TER
SQ SEQUENCE 874 AA; 96254 MW; 97AB8294CE2BA7CA CRC64;

Query Match 52.1%; Score 50; DB 2; Length 874;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GINWNGSGTG 10
Db 749 GINWNGSSG 758

RESULT 16
Q9U234 CABEL PRELIMINARY; PRT; 767 AA.
ID Q9U234 CABEL PRELIMINARY; PRT; 767 AA.
AC Q9U234;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y56A3A.30.
GN ORFNames=Y56A3A.30;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL132860; CAB60506.1; -; Genomic_DNA.
DR Ensembl; Y56A3A.30; Caenorhabditis elegans.
DR WormBase; WBGene00013242; Y56A3A.30.
DR WormPep; Y56A3A.30; CE22595.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 767 AA; 84076 MW; B8D9E3C32EE8CA08 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 767;
Best Local Similarity 47.1%; Pred. No. 85;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GINWNGSGTGADSVKG 17
Db 718 GYGGGGTGYMDNLVG 734

RESULT 17
Q5LD46 BACFN PRELIMINARY; PRT; 1089 AA.
, ID Q5LD46 BACFN PRELIMINARY; PRT; 1089 AA.

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AC Q5LD46;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative exported protein.
GN OrderedLocusNames=BF2270;
OS Bacteroides fragilis (strain ATCC 25285./ NCTC 9343).
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
CA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Poxtan I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
RT gene expression.";
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH07964.1; -; Genomic_DNA.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR InterPro; IPR012910; Plug.
DR InterPro; IPR000531; TonB_receptor.
DR Pfam; PF07715; Plug; 1.
DR Pfam; PF00593; TonB_dep_Rec; 1.
DR PROSITE; PS00175; PG_MUTASE; UNKNOWN 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 1089 AA; 121176 MW; 2446B902BA72B02 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 1089;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 INWNGSGTGAD 13
Db 532 LSMWNGGAAGYSE 543

RESULT 38
Q64U63 BACPR PRELIMINARY; PRT; 1089 AA.
ID Q64U63 BACPR PRELIMINARY; PRT; 1089 AA.
AC Q64U63;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative outer membrane protein involved in nutrient binding.
GN OrderedLocusNames=BF2219;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
CA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuwara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
DR EMBL; AP006841; BA048966.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR InterPro; IPR000531; TonB_receptor.
DR Pfam; PF00593; TonB_dep_Rec; 1.
DR PROSITE; PS00175; PG_MUTASE; UNKNOWN 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 1089 AA; 121203 MW; CDDA56B4FFDFD3 CRC64;

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Query Match 51.0%; Score 49; DB 2; Length 1089;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 INWNGSTGYAD 13
DB 532 LSNWGGAGYSE 543

RESULT 39
HV02 CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region MOO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP PROTEIN SEQUENCE OF 1-112.
RX MEDLINE=77242268; PubMed=407924;
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RT immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP PROTEIN SEQUENCE OF 113-117.
RX MEDLINE=80077682; PubMed=117299; DOI=10.1016/0161-5890(79)90119-6;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
CC -I- MISCELLANEOUS: This mu chain was isolated from a myeloma protein.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A90403; MHGDMO.
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 116 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 50.5%; Score 48.5; DB 1; Length 117;
Best Local Similarity 45.5%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 GINW-----NGSGTGYADSVK 17
DB 44 GLQWADISSGGTYADAVKG 65

RESULT 40
Q6B743_RABIT
ID Q6B743 RABIT PRELIMINARY; PRT; 99 AA.
AC Q6B743;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Immunoglobulin heavy chain variable region (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand;
RX PubMed=15623575; DOI=10.1084/jem.20041849;
RA Rhee K.-J., Jasper P.J., Sethupathi P., Shanmugam M., Lanning D.,
RA Knight K.L.;
RT "Positive selection of the peripheral B cell repertoire in gut-
RT associated lymphoid tissues.";
RL J. Exp. Med. 201:55-62(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand;
RA Rhee K.-J., Jasper P.J., Sethupathi P., Knight K.L.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY676730; AAT91164.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 10730 MW; 272E48650ADBIC1AB CRC64;

Query Match 50.0%; Score 48; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GINWNGSGTGYADSVK 16
DB 51 GFIWGGSTGYADSVK 66

Search completed: November 18, 2005, 21:14:31
Job time : 225.393 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:17:08 ; Search time 136.58 Seconds
(without alignments)
791.381 Million cell updates/sec

Title: US-10-029-926D-208
Perfect score: 1303
Sequence: 1 MEVQLVSGGGVVRFGGSLR.....VVFGGGLTKLTVLGGGCKRAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*
1: Geneseqp19808:*
2: Geneseqp19908:*
3: Geneseqp20008:*
4: Geneseqp20018:*
5: Geneseqp20028:*
6: Geneseqp20038:*
7: Geneseqp20038b:*
8: Geneseqp20048:*
9: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1303	100.0	246	5	Abg78329 Human Fv
2	1303	100.0	246	5	Abg92026 Antibody
3	1273	97.7	256	5	Abg78334 Human Fv
4	1273	97.7	256	5	Abg92025 Antibody
5	1260.5	96.7	266	5	Abg92020 Human ant
6	1257	96.5	277	5	Abg78150 Human Fv
7	1257	96.5	277	5	Abg91841 Human ant
8	1253	96.2	277	8	Adi28366 Human scf
9	1253	96.2	277	8	Adi28366 Human pla
10	1233	94.6	277	5	Abg78328 Human Fv
11	1233	94.6	277	5	Abg92019 Human ant
12	1218.5	93.5	239	5	Abp44926 Human Bly
13	1218.5	93.5	239	7	Adg95753 Single ch
14	1215	93.2	244	9	Adw90315 Phage scf
15	1215	93.2	244	9	Adw90315 SARS coro
16	1214.5	93.2	278	8	Adi28367 Human scf
17	1214.5	93.2	278	8	Adi28367 Human pla
18	1212.5	93.1	239	5	Abp46027 Human Bly
19	1212.5	93.1	239	7	Adg96854 Single ch
20	1210.5	92.9	280	8	Adi28363 P-selecti
21	1210.5	92.9	280	8	Adi28363 Human scf
22	1205.5	92.5	280	9	Adi28363 Amino aci
23	1205.5	92.5	280	9	Adi28363 Single ch
24	1203.5	92.4	280	8	Adi28368 Human scf

25	1203.5	92.4	280	8	Adi28368 Human leu
26	1196.5	91.8	280	9	Adx01181 Amino aci
27	1196.5	91.8	280	9	Adx01130 Amino aci
28	1196.5	91.8	280	9	Ady78324 Single ch
29	1196.5	91.8	280	9	Ady78375 Single ch
30	1195.5	91.7	280	9	Adx01185 Amino aci
31	1195.5	91.7	280	9	Ady78379 Single ch
32	1192.5	91.5	280	9	Adx01186 Amino aci
33	1192.5	91.5	280	9	Ady78380 Single ch
34	1191.5	91.4	239	5	Abp46004 Human Bly
35	1191.5	91.4	239	7	Adg96831 Single ch
36	1191.5	91.4	280	9	Adx01180 Amino aci
37	1191.5	91.4	280	9	Ady78374 Single ch
38	1181	90.6	238	3	Aay95198 Anti-plac
39	1178	90.4	244	6	Aao31136 Human CMO
40	1178	90.4	244	9	Ady34209 TRAIL rec
41	1178	90.4	309	2	Aaw83322 Single ch
42	1178	90.4	309	5	Abb09603 Amino aci
43	1178	90.4	309	6	Abg74384 Single ch
44	1178	90.4	309	7	Adg98737 Human sin
45	1178	90.4	309	8	Ado40446 Human sin

ALIGNMENTS

RESULT 1
ABG78329
ID ABG78329 standard; protein; 246 AA.

XX AC ABG78329;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #204.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KW lymphoma; myeloma; blastoma; melanoma; acute myeloid leukaemia.

XX OS Homo sapiens.

XX PN WO200252664-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

XX PR 29-DEC-2000; 2000US-00751181.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX PI Plaksain D, Peretz T;

XX DR WPI; 2002-619166/66.

XX XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX PT or fragment, or construct of fragment with enhanced binding
XX PT characteristics so as to selectively bind target cell in favor of other
XX PT cells.

XX PS Disclosure; Page 44-45; 232pp; English.

XX CC The invention relates to a peptide or polypeptide comprising an Fv
XX CC molecule, a construct or fragments or a construct of a fragment with
XX CC enhanced binding characteristics which selectively and/or specifically
XX CC binds to a target cell in favour of other cells, where binding is
XX CC primarily determined by a first hypervariable region and Fv is a single
XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX CC association with or attached, coupled, combined, linked or fused to a
XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where
XX CC the medicament has activity against a diseased cell, preferably a cancer

CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX

SQ Sequence 246 AA;

Query Match 100.0%; Score 1303; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEVLVESGGGVVRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTG 60
Db 1 MEVLVESGGGVVRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTG 60
Qy 61 YADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCARMPAVTWGGTTLTVSRGGGG 120
Db 61 YADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCARMPAVTWGGTTLTVSRGGGG 120
Qy 121 SGGGGSGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYVK 180
Db 121 SGGGGSGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYVK 180
Qy 181 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVVFGGTKLTVLGG 240
Db 181 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVVFGGTKLTVLGG 240
Qy 241 GGCKAK 246
Db 241 GGCKAK 246

RESULT 2

ABG92026
ID ABG92026 standard; protein; 246 AA.

XX AC ABG92026;

XX DT 04-DEC-2002 (first entry)

XX DE Antibody protein #5.

XX KW Antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.

XX OS Unidentified.

XX PN WO200253700-A2.

XX PD 11-JUL-2002.

XX PF 31-DEC-2001; 2001WO-US049442.

XX PR 29-DEC-2000; 2000US-00751181.

XX PR 29-DEC-2000; 2000US-0258948P.

XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;

XX PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

XX DR WPI; 2002-674776/72.

XX PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.

PS Disclosure; Fig 52; Opp; English.

XX The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC epitope or its binding fragment having a first hypervariable region. The
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents an antibody protein of the
CC invention

XX SQ Sequence 246 AA;

Query Match 100.0%; Score 1303; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEVLVESGGGVVRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTG 60
Db 1 MEVLVESGGGVVRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTG 60
Qy 61 YADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCARMPAVTWGGTTLTVSRGGGG 120
Db 61 YADSVKGRFTISRDNKNSLYLQNSLRADTAVVYCARMPAVTWGGTTLTVSRGGGG 120
Qy 121 SGGGGSGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYVK 180
Db 121 SGGGGSGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYVK 180
Qy 181 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVVFGGTKLTVLGG 240
Db 181 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVVFGGTKLTVLGG 240
Qy 241 GGCKAK 246
Db 241 GGCKAK 246

RESULT 3

ABG78334

ID ABG78334 standard; protein; 256 AA.

XX AC ABG78334;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #209.

XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.

XX PN WO200259264-A2.

XX PD 01-AUG-2002.

XX PF 31-DEC-2001; 2001WO-US049440.

```
PR 29-DEC-2000; 2000US-00751181.
XX (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
PI Plaksin D, Peretz T;
XX WPI; 2002-619166/66.
XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
PT or fragment, or construct of fragment with enhanced binding
PT characteristics so as to selectively bind target cell in favor of other
PT cells.
XX
PS Example 9; Page 90; 232pp; English.
XX The invention relates to a peptide or polypeptide comprising an Fv
CC molecule, a construct or fragments or a construct of a fragment with
CC enhanced binding characteristics which selectively and/or specifically
CC binds to a target cell in favour of other cells, where binding is
CC primarily determined by a first hypervariable region and Fv is a single
CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
CC association with or attached, coupled, combined, linked or fused to a
CC pharmaceutical agent, is useful in the manufacture of a medicament, where
CC the medicament has activity against a diseased cell, preferably a cancer
CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
CC composition for use in inhibiting the growth of a diseased or cancer
CC cell. This sequence represents a human Fv molecule hypervariable region
CC related peptide of the invention
XX
SQ Sequence 256 AA;
Query Match 97.7%; Score 1273; DB 5; Length 256;
Best Local Similarity 99.6%; Pred. No. 2.1e-80;
Matches 241; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLWVSGINWNGSGTG 60
DB 1 MEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLWVSGINWNGSGTG 60
QY 61 YADSVKGRFTISRDNKNSLYLQMNSLRLEDTAIVYCARMRAPVINGQGTLVTVSRGGGG 120
DB 61 YADSVKGRFTISRDNKNSLYLQMNSLRLEDTAIVYCARMRAPVINGQGTLVTVSRGGGG 120
QY 121 SCGGSGGGGGSSSELTQDPAVSVVALGQTVRITCGDLSRLSYASWYQKQPQAPVLVIYK 180
DB 121 SCGGSGGGGGSSSELTQDPAVSVVALGQTVRITCGDLSRLSYASWYQKQPQAPVLVIYK 180
QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLTVLGG 240
DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLTVLGG 240
QY 241 GG 242
DB 241 GG 242
RESULT 4
ABG92025 standard; protein; 256 AA.
XX
XX ABG92025;
XX
XX 04-DEC-2002 (first entry)
XX Antibody biotag #1.
XX Antibody; antibody biotag; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
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sulphated tyrosine-dependent protein-prbtein interaction.

Unidentified.

WO200253700-A2.

11-JUL-2002.

31-DEC-2001; 2001WO-US049442.

29-DEC-2000; 2000US-00751181.

29-DEC-2000; 2000US-0258948P.

(BIOT-) BIO-TECHNOLOGY GEN CORP.

Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
Szanton E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;

WPI; 2002-674776/72.

Novel isolated epitope present on cancer cells and important in
physiological phenomena such as cell rolling, metastasis and
inflammation, for treating autoimmune, inflammatory or cardiovascular
diseases, and cancer.

Disclosure; Fig 51; Opp; English.

The invention relates to an isolated epitope present on cancer cells and
important in physiological phenomena such as cell rolling, metastasis and
inflammation, where the epitope is capable of being bound by an antibody,
its antigen-binding fragment or its complex comprising at least one
antibody or its binding fragment having a first hypervariable region. The
epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
disease, thrombosis, restenosis, metastasis, growth and/or replication of
tumour or leukaemia cells, increase in number of tumour or leukaemia
cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
platelet and/or cell-platelet adhesion or aggregation, for increasing
mortality of tumour or leukaemia cells, for increasing the susceptibility
of diseased cells to damage by anti-disease, anti-cancer or anti-
leukaemia agents, or for decreasing the number of tumour or leukaemia
cells in a patient, or in the manufacture of a medicament for the above
mentioned purposes. The epitopes are useful for diagnosing and treating
diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
diseases, cardiovascular diseases, such as myocardial infarction,
retinopathic diseases and other diseases mediated by abnormal platelet
function and diseases caused by sulphated tyrosine-dependent protein-
protein interactions. This sequence represents an antibody biotag used in
the scope of the invention

Sequence 256 AA;

Query Match 97.7%; Score 1273; DB 5; Length 256;

Best Local Similarity 99.6%; Pred. No. 2.1e-80; Indels 0; Gaps 0;
Matches 241; Conservative 1; Mismatches 0;

QY 1 MEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLWVSGINWNGSGTG 60

DB 1 MEVQLVESGGGVVRRPGGSLRLSCAASGFTFDDYGMNWVRQAPGKGLWVSGINWNGSGTG 60

QY 61 YADSVKGRFTISRDNKNSLYLQMNSLRLEDTAIVYCARMRAPVINGQGTLVTVSRGGGG 120

DB 61 YADSVKGRFTISRDNKNSLYLQMNSLRLEDTAIVYCARMRAPVINGQGTLVTVSRGGGG 120

QY 121 SCGGSGGGGGSSSELTQDPAVSVVALGQTVRITCGDLSRLSYASWYQKQPQAPVLVIYK 180

DB 121 SCGGSGGGGGSSSELTQDPAVSVVALGQTVRITCGDLSRLSYASWYQKQPQAPVLVIYK 180

QY 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLTVLGG 240

DB 181 NNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLTVLGG 240

QY 241 GG 242

DB 241 GG 242

Db 241 GG 242

RESULT 5
ABG92020
ID ABG92020 standard; protein; 266 AA.

XX AC ABG92020;
XX DT 04-DEC-2002 (first entry)
XX DE Human antibody fragment #204.
XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
XX KW metastasis; hypervariable region; autoimmune disease; thrombosis;
XX KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
XX KW myocardial infarction; retinopathic disease; abnormal platelet function;
XX KW sulphated tyrosine-dependent protein-protein interaction.
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX PD 11-JUL-2002.
XX PF 31-DEC-2001; 2001WO-US049442.
XX PR 29-DEC-2000; 2000US-00751181.
XX PR 29-DEC-2000; 2000US-0258948P.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Lazarovits J, Hagai Y, Plaksin D, Vogel T, Nimrod A, Mar-Haim H;
XX PI Szanthon E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX DR WPI; 2002-674776/72.
XX PT Novel isolated epitope present on cancer cells and important in
XX PT physiological phenomena such as cell rolling, metastasis and
XX PT inflammation, for treating autoimmune, inflammatory or cardiovascular
XX PT diseases, and cancer.
XX PS Disclosure; Page 309-310; 0pp; English.

CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia
CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction,
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention

XX SQ Sequence 266 AA;

Query Match 96.7%; Score 1260.5; DB 5; Length 266;
Best Local Similarity 98.4%; Pred. No. 1.6e-79;
Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSTGY 61

Db 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSTGY 82
QY 62 ADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPVINGOGTLVTVSRGGGGS 121
Db 83 ADSVKGRFTISRDNKNSLYLQNNSLRAEDTAVYYCARMRAPVINGOGTLVTVSRGGGGS 142
QY 122 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLSRYASWYQQKPGQAPVLIYGN 181
Db 143 GGGSGGGGSSSELTQDPAVSVALGQTVRITCGDSLSRYASWYQQKPGQAPVLIYGN 202
QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGGG 241
Db 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVL- 261
QY 242 GCKAK 246
Db 262 AAKAK 266

RESULT 6
ABG78150
ID ABG78150 standard; protein; 277 AA.
XX AC ABG78150;
XX DT 15-NOV-2002 (first entry)
XX DE Human Fv molecule hypervariable region related peptide #25.
XX KW Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
XX KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
XX KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
XX OS Homo sapiens.
XX PN WO20025264-A2.
XX PD 01-AUG-2002.
XX PF 31-DEC-2001; 2001WO-US049440.
XX PR 29-DEC-2000; 2000US-00751181.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;
XX PI Plaksin D, Peretz T;
XX DR WPI; 2002-619166/66.
XX PT Novel peptide/polypeptide for cancer therapy has Fv molecule, construct
XX PT or fragment, or construct of fragment with enhanced binding
XX PT characteristics so as to selectively bind target cell in favor of other
XX PS cells.
XX CC Claim 4; Page 155-156; 232pp; English.
XX CC The invention relates to a peptide or polypeptide comprising an Fv
XX CC molecule, a construct or fragments or a construct of a fragment with
XX CC enhanced binding characteristics which selectively and/or specifically
XX CC binds to a target cell in favour of other cells, where binding is
XX CC primarily determined by a first hypervariable region and Fv is a single
XX CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in
XX CC association with or attached, coupled, combined, linked or fused to a
XX CC pharmaceutical agent, is useful in the manufacture of a medicament, where
XX CC the medicament has activity against a diseased cell, preferably a cancer
XX CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
XX CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an
XX CC acute myeloid leukaemia cell). The peptide is also useful for preparing a
XX CC composition for use in inhibiting the growth of a diseased or cancer
XX CC cell. This sequence represents a human Fv molecule hypervariable region
XX CC related peptide of the invention

XX SQ Sequence 277 AA;

Query Match 96.5%; Score 1257; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3e-79;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVLVESGGVVRPGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGSTGY 61
DB 23 EVLVESGGVVRPGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGSTGY 82

QY 62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAVYYCARMRAPVWQGTLTVTVRSGGGS 121
DB 83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAVYYCARMRAPVWQGTLTVTVRSGGGS 142

QY 122 GGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYGKN 181
DB 143 GGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYGKN 202

QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFSGGTKLTVLG 239
DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFSGGTKLTVLG 260

RESULT 7
ABG91841
ID ABG91841 standard; protein; 277 AA.
XX AC ABG91841;
DT 04-DEC-2002 (first entry)
XX DE Human antibody fragment #25.
XX KW Human; antibody; epitope; cancer; tumour; cell rolling; inflammation;
KW metastasis; hypervariable region; autoimmune disease; thrombosis;
KW restenosis; leukaemia; inflammatory disease; cardiovascular disease;
KW myocardial infarction; retinopathic disease; abnormal platelet function;
KW sulphated tyrosine-dependent protein-protein interaction.
XX OS Homo sapiens.
XX PN WO200253700-A2.
XX PD 11-JUL-2002.
XX PF 31-DEC-2001; 2001WO-US049442.
XX PR 29-DEC-2000; 2000US-00751181.
XX PR 29-DEC-2000; 2000US-0258948P.
XX PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
XX PI Lazarovits J, Hagai Y, Plakain D, Vogel T, Nimrod A, Mar-Haim H;
PI Ssanthou E, Richter T, Amit B, Kooperman L, Peretz T, Levanon A;
XX WPI; 2002-674776/72.
XX PT Novel isolated epitope present on cancer cells and important in
PT physiological phenomena such as cell rolling, metastasis and
PT inflammation, for treating autoimmune, inflammatory or cardiovascular
PT diseases, and cancer.
XX PS Claim 23; Page 233-234; Opp; English.
XX CC The invention relates to an isolated epitope present on cancer cells and
CC important in physiological phenomena such as cell rolling, metastasis and
CC inflammation, where the epitope is capable of being bound by an antibody,
CC its antigen-binding fragment or its complex comprising at least one
CC antibody or its binding fragment having a first hypervariable region. The
CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune
CC disease, thrombosis, restenosis, metastasis, growth and/or replication of
CC tumour or leukaemia cells, increase in number of tumour or leukaemia

CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-
CC platelet and/or cell-platelet adhesion or aggregation, for increasing
CC mortality of tumour or leukaemia cells, for increasing the susceptibility
CC of diseased cells to damage by anti-disease, anti-cancer or anti-
CC leukaemia agents, or for decreasing the number of tumour or leukaemia
CC cells in a patient, or in the manufacture of a medicament for the above
CC mentioned purposes. The epitopes are useful for diagnosing and treating
CC diseases such as cancer, leukaemia, autoimmune diseases, inflammatory
CC diseases, cardiovascular diseases such as myocardial infarction, platelet
CC retinopathic diseases and other diseases mediated by abnormal platelet
CC function and diseases caused by sulphated tyrosine-dependent protein-
CC protein interactions. This sequence represents a human antibody fragment
CC of the invention
XX SQ Sequence 277 AA;

Query Match 96.5%; Score 1257; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 3e-79; 0; Indels 0; Gaps 0;
Matches 238; Conservative 0; Mismatches 0;

QY 2 EVLVESGGVVRPGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGSTGY 61
DB 23 EVLVESGGVVRPGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGSTGY 82

QY 62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAVYYCARMRAPVWQGTLTVTVRSGGGS 121
DB 83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAVYYCARMRAPVWQGTLTVTVRSGGGS 142

QY 122 GGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYGKN 181
DB 143 GGGGGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLYGKN 202

QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFSGGTKLTVLG 239
DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFSGGTKLTVLG 260

RESULT 8
AD128366
ID AD128366 standard; protein; 277 AA.
XX AC AD128366;
XX DT 06-MAY-2004 (first entry)
XX DE Human scFv fragment Y1, binds to platelets.
XX KW Human; antibody; scFv; platelet; drug delivery; cancer; therapy.
XX OS Homo sapiens.
XX PN WO2004002528-A1.
XX PD 08-JAN-2004.
XX PF 30-JUN-2003; 2003WO-US020604.
XX PR 01-JUL-2002; 2002US-00189025.
XX PA (SAVI-) SAVIENT PHARM INC.
XX PI Lazarovits J, Nimrod A, Hoch-Mar-Chaim H, Levanon A;
XX WPI; 2004-099189/10.
XX PT Composition comprising an agent and/or antibody or its fragment, useful
PT for treating autoimmune disease, thrombosis, restenosis, metastasis, or
PT for inhibiting growth and/or replication of tumor cells or leukemia
PT cells.
XX PS Claim 13; SEQ ID NO 1; 58pp; English.
XX XX The present sequence is the protein sequence of human scFv fragment Y1.

CC This antibody was identified by screening a human antibody phage library
CC that has diversity only in the heavy chain CDR3 regions. Fixed human
CC platelets were screened in order to identify antibodies that bind
CC platelets. The epitope for Y1 antibody is located between amino acids 272
CC and 285 on glyocalicin, a subunit of the CD42 complex. Y1 also binds the
CC N-terminal of P8GL-1, a receptor for E-, L- and P-selectins, and has a
CC high affinity for primary leukaemia cells. The invention relates to
CC compositions utilising an agent and an antibody or its fragment. The
CC agent is a toxin, radioisotope or pharmaceutical agent such as
CC doxorubicin. It is complexed or combined with or conjugated to the
CC antibody or its fragment. The agent and/or antibody can be present in the
CC composition as a sub-clinical amount, i.e. less than the amount generally
CC found to be clinically effective when the agent is administered alone.
CC The composition is used in claimed methods of: inhibiting cell rolling,
CC inflammation, thrombosis, restenosis, metastasis, the growth and/or
CC replication of tumour cells or leukaemia cells, an increase in number of
CC tumour or leukaemia cells, cell-cell, cell-matrix, platelet-matrix,
CC platelet-platelet and/or cell-platelet complex formation, aggregation or
CC adhesion; increasing the mortality rate of tumour or leukaemia cells, the
CC susceptibility of disease cells to damage by anti-disease agents, and the
CC susceptibility of tumour or leukaemia cells to damage by anti-cancer
CC agents; and ameliorating the effects of a disease, preventing a disease,
CC treating a disease or inhibiting the progress of a disease.

XX Sequence 277 AA;

Query Match 96.2%; Score 1253; DB 8; Length 277;
Best Local Similarity 99.6%; Pred. No. 5.7e-79;
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVWRQAPGKGLVWSGNNWGGSTGY 61
DB 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVWRQAPGKGLVWSGNNWGGSTGY 82
QY 62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLLTVSRGGGGS 121
DB 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLLTVSRGGGGS 142
QY 122 GGGSGGGGSELTPDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLIYIGN 181
DB 143 GGGSGGGGSELTPDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLIYIGN 202
QY 182 NRPSSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 239
DB 203 NRPSSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 260

RESULT 9
ADS82026

XX AD82026 standard; protein; 277 AA.

XX AC ADS82026;

XX DT 30-DEC-2004 (first entry)

XX DE Human platelet binding scFv antibody fragment Y1.

XX cell rolling; inflammation; autoimmune disease; thrombosis; restenosis;
KW metastasis; tumour; leukaemia; cardiovascular disease; retinopathy;
KW human; scFv; antibody; cytostatic; antiinflammatory; thrombolytic;
KW vasotrophic; immunosuppressive; cardiovascular-Gen; ophthalmological.

XX OS Homo sapiens.

XX FN US2004202665-A1.

XX PD 14-OCT-2004.

XX PF 30-JUN-2003; 2003US-00610843.

XX PR 01-JUL-2002; 2002US-0393453P.

XX (LAZA/) LAZAROVITS J.

PA (NIMR/) NIMROD A.
PA (HOCH/) HOCH M H.
PA (LEVA/) LEVANON A.

PI Lazarovits J, Nimrod A, Hoch MH, Levanon A;

XX WPI; 2004-746943/73.

DR Composition useful for treating diseases e.g., inflammatory diseases,
XX thrombosis, restenosis, autoimmune diseases, cardiovascular diseases or
XX retinopathic diseases, comprises agent and antibody or its fragment.

XX Claim 13; SEQ ID NO 1; 22pp; English.

CC The invention relates to a composition which comprises an agent and an
CC antibody or its fragment. The composition is useful for inhibiting cell
CC rolling, inflammation, autoimmune disease, thrombosis, restenosis,
CC metastasis, cell-cell, cell-matrix, platelet-matrix, platelet-platelet
CC and/or cell-platelet complex formation, aggregation or adhesion, increase
CC in number of tumour cells or growth and/or replication of tumour or
CC leukaemia cells, for increasing the mortality rate of tumour or leukaemia
CC cells, the susceptibility of tumour or leukaemia cells to damage by anti-
CC cancer agents, for decreasing number of tumour or leukaemia cells, or for
CC ameliorating the effect of a disease, preventing a disease, treating a
CC disease, or inhibiting the progress of a disease. The composition is
CC useful for therapeutic treatment, where antibody or its fragment and the
CC agent are administered separately. The antibody or its fragment is
CC administered prior to or subsequent to the agent. The composition is
CC useful for treating diseases such as inflammatory diseases, diseases
CC involving abnormal or pathogenic adhesion, thrombosis and/or restenosis,
CC diseases involving abnormal or pathogenic aggregation, autoimmune
CC diseases, cardiovascular diseases, retinopathic diseases, diseases caused
CC by sulphated tyrosine-dependent protein-protein interactions or diseased
CC cells. The present sequence represents the human platelet binding scFv
CC antibody fragment Y1.

XX Sequence 277 AA;

Query Match 96.2%; Score 1253; DB 8; Length 277;
Best Local Similarity 99.6%; Pred. No. 5.7e-79;
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVWRQAPGKGLVWSGNNWGGSTGY 61

DB 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVWRQAPGKGLVWSGNNWGGSTGY 82

QY 62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLLTVSRGGGGS 121

DB 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLLTVSRGGGGS 142

QY 122 GGGSGGGGSELTPDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLIYIGN 181

DB 143 GGGSGGGGSELTPDPAVSVALGQTVRITCGDLSRYSYASWYQKPGQAPVLIYIGN 202

QY 182 NRPSSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 239

DB 203 NRPSSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 260

RESULT 10
ABG78328

ID ABG78328 standard; protein; 277 AA.

XX AC ABG78328;

XX DT 15-NOV-2002 (first entry)

XX DE Human Fv molecule hypervariable region related peptide #203.

XX Human; Fv molecule; hypervariable region; single chain Fv; cytostatic;
KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

|||||
203 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLG 260
|||||
RESULT 12
ABP44926
ID ABP44926 standard; protein; 239 AA.
XX AC ABP44926;
XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 937.
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-0277379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX Claim 1; Page 1520-1521; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX Sequence 239 AA;
Query Match 93.5%; Score 1218.5; DB 5; Length 239;
Best Local Similarity 97.9%; Pred. NO. 1.2e-76;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
2 EQVLVESGGGVVRPGGSLRLSCAASGFTFDYDYGMSWVRQAPGKLEWVSGINWNGSGTGY 61
|||||

Db 1 EQVLVESGGGVVRPGGSLRLSCAASGFTFDYDYGMSWVRQAPGKLEWVSGINWNGSGTGY 60
QY 62 ADSVKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARMR-APVITWGOGTLVTVSRGGGG 120
|||||
Db 61 ADSVKGRFTTISRDNKNSLYLQNNSLRAEDTAVYYCARRRVALDYWGOGTLVTVSRGGGG 120
QY 121 SGGGSGGGSSSELTQDPVAVSVALGQTVRITCQGDSLRSYYASWYQKPGQAPVLVIYVK 180
Db 121 SGGGSGGGSSSELTQDPVAVSVALGQTVRITCQGDSLRSYYASWYQKPGQAPVLVIYVK 180
QY 181 NNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLG 239
Db 181 NNRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTKLTVLG 239
RESULT 13
ADG95753
ID ADG95753 standard; protein; 239 AA.
XX AC ADG95753;
XX DT 11-MAR-2004 (first entry)
XX DE Single chain antibody that immunospecifically binds BlyS SeqID 937.
XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX Unidentified.
XX OS WO2003055979-A2.
XX PN 10-JUL-2003.
XX PD 14-NOV-2002; 2002WO-US036496.
XX PF 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (BlyS), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX Example 1; SEQ ID NO 937; 394pp; English.
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey BlyS. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of BlyS or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antirheumatic, antiarthritic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
XX polypeptide sequence is a single chain antibody that binds BlyS of the

CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ffp.wipo.int/pub/published pct_sequences.

XX SQ Sequence 239 AA;
Query Match 93.5%; Score 1218.5; DB 7; Length 239;
Best Local Similarity 97.9%; Pred. No. 1.2e-76;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 2 EVLVESGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINWNGSTGY 61
DB 1 EVLVESGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINWNGSTGY 60
QY 62 ADSVKGRFTISRDNKNSLYLQNSLRADTAIVYICARMR-APVINGOGTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNKNSLYLQNSLRADTAIVYICARRRYALDYWGQGTLVTVSRGGG 120
QY 121 SGGGGGGGGSSSLTQDPVAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLIYVK 180
DB 121 SGGGGGGGGSSSLTQDPVAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLIYVK 180
QY 181 NRPSPGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 239
DB 181 NRPSPGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 239

RESULT 14
ADW90315
ID ADW90315 standard; protein; 244 AA.
XX AC ADW90315;
XX DT 21-APR-2005 (first entry)
XX DE Phage scFV SARS antibody SEQ ID NO 585.
XX KW Virucide; Vaccine; diagnosis; Severe acute respiratory syndrome;
XX KW respiratory-gen.; infection; respiratory disease; antibody.

XX OS SARS coronavirus.
XX PN WO2005012337-A2.
XX PD 10-FEB-2005.
XX PF 15-JUL-2004; 2004WO-EP051498.
XX PR 15-JUL-2003; 2003WO-EP050308.
XX PR 24-JUL-2003; 2003WO-EP050333.
XX PR 02-SEP-2003; 2003WO-EP050392.
XX PR 27-OCT-2003; 2003WO-EP050761.
XX PR 24-NOV-2003; 2003WO-EP050883.
XX PA (CRUC-) CRUCELL HOLLAND BV.
XX PI Ter Meulen JH, Goudsmit J, Slootstra JW, Timmerman P, De Kruif CA;
XX PI Van Den Brink EN;
XX WPI; 2005-162947/17.

PT New antigenic peptides from severe acute respiratory syndrome-coronavirus
PT (SARS-CoV), useful in preparing a composition for diagnosing, treating or
PT preventing SARS-CoV infection.

XX Example 2; SEQ ID NO 585; 199pp; English.

XX The invention relates to an antigenic peptide from severe acute
CC respiratory syndrome-coronavirus (SARS-CoV). The peptide or nucleic acid
CC molecule encoding the peptide, fusion protein, conjugate or antibody is
CC useful in preparing a composition for diagnosing, treating or preventing
CC SARS-CoV infection. The present sequence represents a phase scFV SARS
CC antibody.

XX SQ Sequence 244 AA;
Query Match 93.2%; Score 1215; DB 9; Length 244;
Best Local Similarity 97.5%; Pred. No. 2.1e-76;
Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 EVLVESGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINWNGSTGY 61
DB 4 EVLVESGGVVRPGGSLRLSCAASGFTFDDYGMWVRQAPGKLEWVSGINWNGSTGY 63
QY 62 ADSVKGRFTISRDNKNSLYLQNSLRADTAIVYICARMR-APVINGOGTLVTVSRGGG 121
DB 64 ADSVKGRFTISRDNKNSLYLQNSLRADTAIVYICARGLSLRPPWQGTLVTVSRGGG 123
QY 122 GGGGGGGGGSSSLTQDPVAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLIYVK 181
DB 124 GGGGGGGGGSSSLTQDPVAVSVALGQTVRITTCGDSLSRYASWYQKPGQAPVLIYVK 183
QY 182 NRPSPGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 239
DB 184 NRPSPGIPDRFGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGKTLTVLG 241

RESULT 15
ADX01815
ID ADX01815 standard; protein; 244 AA.

XX AC ADX01815;
XX DT 21-APR-2005 (first entry)
XX DE SARS coronavirus scFv antibody SEQ ID NO 71.
XX KW severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
XX KW respiratory disease; infection; antibody.

XX OS SARS coronavirus.
XX PN WO2005012360-A2.
XX PD 10-FEB-2005.
XX PF 21-JUL-2004; 2004WO-EP051568.
XX PR 22-JUL-2003; 2003WO-EP050328.
XX PR 01-SEP-2003; 2003WO-EP050391.
XX PR 16-OCT-2003; 2003WO-EP050723.
XX PR 24-NOV-2003; 2003WO-EP050883.
XX PR 04-DEC-2003; 2003WO-EP050943.
XX PR 02-FEB-2004; 2004WO-EP050067.
XX PR 13-FEB-2004; 2004WO-EP050127.
XX PR 19-MAR-2004; 2004WO-EP050334.
XX PR 07-APR-2004; 2004WO-EP050464.
XX PR 14-APR-2004; 2004WO-EP050516.
XX PR 29-APR-2004; 2004WO-EP050643.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX DR N-PSDB; ADX01814.

XX New binding molecules that specifically bind to severe acute respiratory
PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
PT treating conditions resulting from SARS-CoV.

XX Example 3; SEQ ID NO 71; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
CC specifically binding to a severe acute respiratory syndrome (SARS)-
CC coronavirus (CoV). The composition (including the binding molecule or its
CC antibody.

CC functional variant, or the immunoconjugate) is useful as a medicament for
CC the diagnosis, prophylaxis or treatment of a condition resulting from a
CC SARS-CoV, or in the preparation of the medicament. The present sequence
CC represents a SARS coronavirus scFv.
XX

8Q Sequence 244 AA;

Query Match 93.2%; Score 1215; DB 9; Length 244;
Best Local Similarity 97.5%; Pred. No. 2.1e-76;
Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAAPKGLEWVSGINWNGGSTGY 61
Db |||||
Qy 4 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAAPKGLEWVSGINWNGGSTGY 63
Db |||||
Qy 62 ADSVKGRFTISRDNKNSLYIQMNSLRAEDTAVYYCARMRAPVTVWGQGLVTVSRGGGGS 121
Db |||||
Qy 64 ADSVKGRFTISRDNKNSLYIQMNSLRAEDTAVYYCARGLSLRPWGQGLVTVSRGGGGS 123
Db |||||
Qy 122 GGGSGGGSGSSELTQDPAVSVALGQTVRITCGDSLSRSYYASWYQQKPGQAPVLIYGN 181
Db |||||
Qy 124 GGGSGGGSGSSELTQDPAVSVALGQTVRITCGDSLSRSYYASWYQQKPGQAPVLIYGN 183
Db |||||
Qy 182 NRPSCIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVPFGGKLTVLG 239
Db |||||
Qy 184 NRPSCIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSGHNHVPFGGKLTVLG 241
Db |||||

Search completed: November 18, 2005, 21:46:18
Job time : 137.58 secs

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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:40:23 ; Search time 33.7571 Seconds
(without alignments)
602.487 Million cell updates/sec

Title: US-10-029-926d-208
Perfect score: 1303
Sequence: 1 MEVLVSGGVVRPGSLR.....VVFGGTKLTVLGGGCKAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/ECTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/baCkfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	90.4	309	2	US-09-079-029-9
2	1098.5	84.3	312	2	US-09-079-029-10
3	1095.5	84.1	280	2	US-09-260-527-1
4	943.5	72.4	278	2	US-09-260-527-3
5	875.5	67.2	310	2	US-09-079-029-11
6	822	63.1	268	2	US-09-976-118-1
7	803	61.6	240	2	US-09-192-854-2
8	803	61.6	240	2	US-09-511-939-2
9	793.5	60.9	334	2	US-09-646-028-53
10	793.5	60.9	339	2	US-09-646-028-55
11	793.5	60.9	348	2	US-09-646-028-51
12	782.5	60.1	288	2	US-09-818-247-22
13	774.5	59.4	245	2	US-08-918-148-75
14	774.5	59.4	245	2	US-09-138-091A-73
15	771.5	59.2	245	2	US-08-918-148-76
16	771.5	59.2	245	2	US-09-138-091A-74
17	768.5	59.0	245	2	US-08-918-148-78
18	768.5	59.0	245	2	US-09-138-091A-76
19	756.5	58.1	281	2	US-09-025-7698-178
20	756.5	58.1	281	2	US-09-025-7698-178
21	756.5	58.1	281	2	US-09-490-070A-178
22	756.5	58.1	281	2	US-09-490-153-178
23	744	57.1	244	2	US-09-490-324-178
24	744	57.1	244	2	US-08-918-148-77
25	726.5	55.8	240	1	US-09-138-091A-75
26	726.5	55.8	240	1	US-08-488-113B-148
27	726.5	55.8	240	1	US-08-477-484B-148

28	726.5	55.8	240	2	US-08-839-765-148	Sequence 148, Appl
29	726.5	55.8	240	2	US-09-136-389-148	Sequence 148, Appl
30	726.5	55.8	240	2	US-09-610-838-148	Sequence 148, Appl
31	726.5	55.8	240	2	US-09-711-485-148	Sequence 148, Appl
32	718.5	55.1	553	1	US-08-661-052-16	Sequence 16, Appl
33	718.5	55.1	553	2	US-09-188-082-16	Sequence 16, Appl
34	718.5	55.1	553	2	US-09-364-088-16	Sequence 16, Appl
35	718.5	55.1	553	2	US-09-102-716-16	Sequence 16, Appl
36	716.5	55.0	301	1	US-08-661-052-14	Sequence 14, Appl
37	716.5	55.0	301	1	US-09-188-082-14	Sequence 14, Appl
38	716.5	55.0	301	2	US-09-364-088-14	Sequence 14, Appl
39	716.5	55.0	301	2	US-09-102-716-14	Sequence 14, Appl
40	707	54.3	236	1	US-08-190-199A-65	Sequence 65, Appl
41	703.5	54.0	284	2	US-08-564-164A-2	Sequence 2, Appl
42	702	53.9	255	2	US-09-553-498-8	Sequence 8, Appl
43	702	53.9	255	2	US-09-618-869-8	Sequence 8, Appl
44	701	53.8	244	2	US-08-918-148-79	Sequence 79, Appl
45	701	53.8	244	2	US-08-138-091A-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-079-029-9

Query Match 90.4%; Score 1178; DB 2; Length 309;
Best Local Similarity 92.2%; Pred. No. 3e-88;
Matches 225; Conservative 5; Mismatches 8; Indels 6; Gaps 1;
QY 2 EVLVSGGVVRPGSLRSCAASGTFDDYQMSVVRQAPGKLEWVGNNNGSTGY 61
DB 40 EVLVSGGVVRPGSLRSCAASGTFDDYQMSVVRQAPGKLEWVGNNNGSTGY 99
QY 62 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYVCARMAP-----VIWGGTTLVTS 115

Db 100 ADSVGRVITSRDIAKNSLYLQMSLRAEDTAVYYCAIKLAGRWYFDLWKGKTTVTS 159
Qy 116 RGGGSGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPVL 175
Db 160 SGGGSGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPVL 219
Qy 176 VIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTTKL 235
Db 220 VIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTTKL 279
Qy 236 TVLG 239
Db 280 TVLG 283

RESULT 2

US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369

GENERAL INFORMATION:

; APPLICANT: Adams, Camilia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029

FILING DATE:

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-079-029-10

Query Match 84.3%; Score 1098.5; DB 2; Length 312;
Best Local Similarity 87.0%; Pred. No. 9.1e-82;
Matches 214; Conservative 5; Mismatches 18; Indels 9; Gaps 1;

Qy 3 VOLVESGGVVRPGGSLRLSCAASGFTFDDYGMVSRQAPGKLEWVSGINWNGSGTGYA 62
Db 41 VOLVESGGGLVQPGGSLRLSCAASGFTFSSYMWVSRQAPGKLEWVANIQDSEKYYV 100
Qy 63 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRPV-----IWGGTTLVT 113
Db 101 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDLLKVKGSSSGWFPWGRGTTVT 160
Qy 114 VSRGGGGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAP 173
Db 161 VSSGGGGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAP 220

Qy 174 VLVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTT 233
Db 221 VLVIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTT 280
Qy 234 KLTVLG 239
Db 281 KLTVLG 286

RESULT 3

US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599

GENERAL INFORMATION:

; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 280
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
; OTHER INFORMATION: phage display library known as the Synthetic scfv
; OTHER INFORMATION: Library (#1) from the Centre for Protein
; OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match 84.1%; Score 1095.5; DB 2; Length 280;

Best Local Similarity 88.4%; Pred. No. 1.4e-81;
Matches 213; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

Qy 2 EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMVSRQAPGKLEWVSGI--NWNNGST 59
Db 23 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMWVSRQAPGKLEWVGRKSKTDGTT 82
Qy 60 GYADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAR-MRAPVTIWGGTTLVTSRGG 118
Db 83 DYAAPVKGRFTISRDSKNTLYLQMSLKTEDTAVYYCARKWKALRWGGTTLVTSRGG 142
Qy 119 GSGGGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPVLVIY 178
Db 143 GSGGGGGGGGGSSSLTQDPVAVSVALGQTVRTTCQGDLSRSYYASWYQKPGQAPVLVIY 202
Qy 179 GKNNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTTKLTVL 238
Db 203 GKNNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSGNNHVVFGGTTKLTVL 262
Qy 239 G 239
Db 263 G 263

RESULT 4

US-09-260-527-3
; Sequence 3, Application US/09260527A
; Patent No. 6228599

GENERAL INFORMATION:

; APPLICANT: Knox, J.P.
; APPLICANT: Mikelsen, J.D.
; APPLICANT: Willats, W. G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DY0U19.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; CURRENT FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3
LENGTH: 278
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected from a naive phage display library known as the
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

Query Match 72.4%; Score 943.5; DB 2; Length 278;
Best Local Similarity 77.1%; Pred. No. 3.3e-69;
Matches 195; Conservative 17; Mismatches 35; Indels 3; Gaps 3;

QY 2 EVLVESGGGVVRPGGSLRLSCAASGFTDDYVMSWVRQAPGKGLVWSGINWNGSGTG 60
Db 23 QVQLQESGPGLVKPSDTLSITCAVSGYSISSNNMGMIRQPPGKGLEWI-GYIYSGSTY 81

QY 61 YADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMRAPVI-WGOGTLVTVSRGG 119
Db 82 YNPSLKSRVTMSVDTSKNQFSLKLSVTAVDTAIVYYCARFPRVYDWGGTLTVSRGG 141

QY 120 GSGGGGGGGGSELQDPAVSVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYG 179
Db 142 GSGGGGGGGGSELQDPAVSVVALGQTVRITCGDLSRYSYASWYQKPGQAPVLVIYG 201

QY 180 KNNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGTKLTVLG 239
Db 202 KNNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGTKLTVLG 261

RESULT 5
US-09-079-029-11
Sequence 11, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: US/09/079, 029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11

Query Match 67.2%; Score 875.5; DB 2; Length 310;
Best Local Similarity 71.8%; Pred. No. 1.3e-63;
Matches 176; Conservative 19; Mismatches 43; Indels 7; Gaps 3;

QY 2 EVLVESGGGVVRPGGSLRLSCAASGFTDDYVMSWVRQAPGKGLVWSGINWNGSGTG 61
Db 40 QVQLVQSGGGVVPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLVWSGINWNGSGTG 99

QY 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMRAPV---IWQGGTLVTVSRGG 118
Db 100 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMRAPV---IWQGGTLVTVSRGG 159

QY 119 GSGGGGGGGGSELQDPAVSVVALGQTVRITCGDLSR---SYASWYQKPGQAPV 174
Db 160 GSGGGGGGGGSELQDPAVSVVALGQTVRITCGDLSR---SYASWYQKPGQAPV 219

QY 175 LVYIKNNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNHVVFGGTK 234
Db 220 LLIYDSDNRPSGVPDRFSGSRGTSASLAITGLQAEADYYCQSYDSSLRSGVFGGTK 279

QY 235 LTVLG 239
Db 280 VTVLG 284

RESULT 6
US-09-976-118-1
Sequence 1, Application US/09976118
Patent No. 6699473
GENERAL INFORMATION:
APPLICANT: Raisch, Kevin Paul
APPLICANT: Curiel, David T.
APPLICANT: Bonner, James Allen
TITLE OF INVENTION: Human Anti-Epidermal Growth Factor Receptor
TITLE OF INVENTION: Single-Chain Antibodies
FILE REFERENCE: D6355
CURRENT APPLICATION NUMBER: US/09/976,118
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,353
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 268
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: amino acid sequence of anti-EGFR scFv
OTHER INFORMATION: clone pSEX81-6
US-09-976-118-1

Query Match 63.1%; Score 822; DB 2; Length 268;
Best Local Similarity 67.3%; Pred. No. 2.4e-59;
Matches 169; Conservative 21; Mismatches 47; Indels 14; Gaps 3;

QY 2 EVLVESGGGVVRPGGSLRLSCAASGFTDDYVMSWVRQAPGKGLVWSGINWNGSGTG 61
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMHWVRQAPGKGLVYSISSNGSGTY 60

QY 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMRAPV-----IWQGGTLV 112
Db 61 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARMRAPV-----IWQGGTLV 120

QY 113 TVSRGGGGS---GGGGGGGGGSELQDPAVSVVALGQTVRITCGDLSRYSYASWYQK 168
Db 121 TVSSGGASAPKLEEGFSEARVSVLTQPPSLVSPQQTASITCSGDKLGDKYASWYQK 180

QY 169 PGQAPVLVIYKNNRPSGIPDRFSGSSGNTASITITGAQAEADYYCNSRDSGNHVV 228
Db 181 PGQSPVLVIYQDRKRPISGIPERFSGNSGNTATLTISGTQAMDEADYYCQAMDSSTPY-V 239

QY 229 FGGGTLVTVLG 239
Db 240 FGTGTVTVLG 250

Best Local Similarity 66.24; Pred. No. 1:5E-58;

GENERAL INFORMATION:

; Sequence 55, Application US/09646028

APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 55
LENGTH: 339
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence./note=synthetic construct
US-09-646-028-55

Query Match 60.9%; Score 793.5; DB 2; Length 339;
Best Local Similarity 63.9%; Pred. No. 6.7e-57; Indels 11; Gaps 4;
Matches 159; Conservative 27; Mismatches 52

QY 1 MEVQLVESGGGVVPRPGGSLRLSCAASGFTPDYCMQSVWRQAPGKGLWVSGINWNGSGTG 60
DB 84 LEVQLVESGGGLVQSGSLRLSCVASGLTFSSSAITWVRQAPGKGLWVSGISFSGDTTY 143
QY 61 YADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYFCARMRAPIV----WGQGTLLTVV-S 115
DB 144 YADSVKGRFSARDNSKNTVYLQNNLRPNDAVYFCANNQTNFCLDNWQGTLLTVSS 203
QY 116 RGGGGSGGGSGGGGS---SELTQDPAVSVLQGTVRITCQGDLSR---SYVASWYQOKP 169
DB 204 RGGGGSGGGSGGGGSQSVLTQPPSVSAAPQQRVTISCTGSRNSIGAGYDVMYQKFP 263
QY 170 GQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYVYCNRRDSSGNHVV 229
DB 264 ETAPKVLIIYNNRRPSGVDRFGSGSGTSSASLAITGLQLEDEGTYYCQCNDDSLGWL 323
QY 230 GGGTKLTVL 238
DB 324 GGGTKLTVL 332

RESULT 11
US-09-646-028-51
Sequence 51, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 51
LENGTH: 348
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence./note=synthetic construct
US-09-646-028-51

Query Match 60.9%; Score 793.5; DB 2; Length 348;
Best Local Similarity 63.9%; Pred. No. 6.9e-57;
Matches 159; Conservative 27; Mismatches 52; Indels 11; Gaps 4;

QY 1 MEVQLVESGGGVVPRPGGSLRLSCAASGFTPDYCMQSVWRQAPGKGLWVSGINWNGSGTG 60

DB 93 LEVQLVESGGGLVQSGSLRLSCVASGLTFSSSAITWVRQAPGKGLWVSGISFSGDTTY 152
QY 61 YADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYFCARMRAPIV----WGQGTLLTVV-S 115
DB 153 YADSVKGRFSARDNSKNTVYLQNNLRPNDAVYFCANNQTNFCLDNWQGTLLTVSS 212
QY 116 RGGGGSGGGSGGGGS---SELTQDPAVSVLQGTVRITCQGDLSR---SYVASWYQOKP 169
DB 213 RGGGGSGGGSGGGGSQSVLTQPPSVSAAPQQRVTISCTGSRNSIGAGYDVMYQKFP 272
QY 170 GQAPVLVIYGNKRRPSGIPDRFGSSSGNTASLTITGAQAEADYVYCNRRDSSGNHVV 229
DB 273 ETAPKVLIIYNNRRPSGVDRFGSGSGTSSASLAITGLQLEDEGTYYCQCNDDSLGWL 332
QY 230 GGGTKLTVL 238
DB 333 GGGTKLTVL 341

RESULT 12
US-09-818-247-22
Sequence 22, Application US/09818247
Patent No. 6855810
GENERAL INFORMATION:
APPLICANT: Mostov, Keith E.
APPLICANT: Chapin, Steven J.
APPLICANT: Richman-Eisenstat, Janice
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Ligands Directed to the No. 6855810-Secretory Component,
TITLE OF INVENTION: No. 6855810-Stalk Region of p19R and Methods of Use Thereof
FILE REFERENCE: 18062E-000910US
CURRENT APPLICATION NUMBER: US/09/818,247
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: WO PCT/US01/09699
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/192,197
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,198
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 288
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence: Pelb/4AF/myc/6HIS
US-09-818-247-22

Query Match 60.1%; Score 782.5; DB 2; Length 288;
Best Local Similarity 65.0%; Pred. No. 4.3e-56;
Matches 158; Conservative 26; Mismatches 50; Indels 9; Gaps 4;

QY 2 EVQLVESGGGVVPRPGGSLRLSCAASGFTPDYCMQSVWRQAPGKGLWVSGINWNGSGTG 61
DB 23 QVQLVQSGGGGVVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSAISGSGSTY 82
QY 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYFCARMRAPIV-----VINGQGTLLTVSR 116
DB 83 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYFCARSFTVNSGYFQHWGQGTLLTVSS 142
QY 117 GGGSGGGSGGGSGGS-ELTQDPA-VSVLQGTVRITCQGDLSRYSYASWYQOKPQAPV 174
DB 143 GGGSGGGSGGGSGGSEIVLTQSPSTLSASIGDRVTITCRASEGIYHHLWYQOKPKAPK 202
QY 175 LVIVGKNNRPSGIPDRFGSSSGNTASLTITGAQAEADYVYCNRRDSSGNHVVFGGK 234
DB 203 LLIYKASSLASGVPSPRFGSGSGTDFLTITSLQPEDFATYYCQHYDST--PPTFGQGTK 260
QY 235 LTV 237

```
Db 261 VDI 263

RESULT 13
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75

Query Match 59.4%; Score 774.5; DB 2; Length 245;
Best Local Similarity 65.1%; Pred. No. 1.6e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 61
Db 3 EVQLVQSGGGLVKPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 62
Qy 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMR---APVIWGQGLTVTVSRGG 118
Db 63 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMWGEDAFDIWGQGTMTVTVSRGG 122
Qy 119 GSGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLV 176
Db 123 GSGGGGGGGGSDIVMTQSPSTLSASVGRVAITCRASEGIVHMLAWYQKPGKAPKLL 182
Qy 177 IYKKNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLT 236
Db 183 IYKASSLASGAPSRFSGSGGADFTLTISLQPDPAFYTC--QQYSNYPLTFGGGTKLE 240
Qy 237 V 237
Db 241 V 241

RESULT 14
US-09-138-091A-73
; Sequence 73, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

Query Match 59.4%; Score 774.5; DB 2; Length 245;
Best Local Similarity 65.1%; Pred. No. 1.6e-55;
Matches 157; Conservative 28; Mismatches 49; Indels 7; Gaps 4;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 61
Db 3 EVQLVQSGGGLVKPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 62
Qy 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMR---APVIWGQGLTVTVSRGG 118
Db 63 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMWGEDAFDIWGQGTMTVTVSRGG 122
Qy 119 GSGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLV 176
Db 123 GSGGGGGGGGSDIVMTQSPSTLSASVGRVAITCRASEGIVHMLAWYQKPGKAPKLL 182
Qy 177 IYKKNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLT 236
Db 183 IYKASSLASGAPSRFSGSGGADFTLTISLQPDPAFYTC--QQYSNYPLTFGGGTKLE 240
Qy 237 V 237
Db 241 V 241

RESULT 15
US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-76

Query Match 59.2%; Score 771.5; DB 2; Length 245;
Best Local Similarity 63.2%; Pred. No. 2.8e-55;
Matches 153; Conservative 31; Mismatches 51; Indels 7; Gaps 4;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 61
Db 3 EVQLVQSGGGLVKPGGSLRLSCAASGFTFDYGMHWVRQAPGKGLVWVSGINWNGSGTGY 62
Qy 62 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMR---APVIWGQGLTVTVSRGG 118
Db 63 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYICARMWGEDAFDIWGQGTMTVTVSRGG 122
Qy 119 GSGGGGGGGGSS-ELTQDPA-VSVALGQTVRITCGDSLSRSYASWYQKPGQAPVLV 176
Db 123 GSGGGGGGGGSDIVMTQSPSTLSASVGRVAITCRASEGIVHMLAWYQKPGKAPKLL 182
Qy 177 IYKKNRPSPGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGTKLT 236
Db 183 IYKASSLASGAPSRFSGSGGADFTLTISLQPDPAFYTC--QQYSNYPLTFGGGTKLE 240
Qy 237 VL 238
Db 241 IL 242

Search completed: November 18, 2005, 21:55:06
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Job time : 34.7571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:47:37 ; Search time 109.42 Seconds
(without alignments)
939.375 Million cell updates/sec

Title: US-10-029-926D-208
Perfect score: 1303
Sequence: 1 MEVLVSGGGVVRPGGSLR.....VVFGGGTLTVLGGGCKAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1260.5	96.7	266	4 US-10-032-037B-204	Sequence 204, App
2	1260.5	96.7	266	4 US-10-029-988B-204	Sequence 204, App
3	1260.5	96.7	266	4 US-10-032-423A-204	Sequence 204, App
4	1257	96.5	277	4 US-10-032-037B-25	Sequence 25, Appl
5	1257	96.5	277	4 US-10-029-988B-25	Sequence 25, Appl
6	1257	96.5	277	4 US-10-032-423A-25	Sequence 25, Appl
7	1257	96.5	277	4 US-10-029-926B-25	Sequence 25, Appl
8	1253	96.2	277	4 US-10-610-843B-1	Sequence 1, Appli
9	1233	94.6	277	4 US-10-032-037B-203	Sequence 203, App
10	1233	94.6	277	4 US-10-029-988B-203	Sequence 203, App
11	1233	94.6	277	4 US-10-032-423A-203	Sequence 203, App
12	1233	94.6	277	4 US-10-029-926B-203	Sequence 203, App
13	1218.5	93.5	239	3 US-09-880-748-937	Sequence 937, App
14	1218.5	93.5	239	3 US-10-293-418-937	Sequence 937, App
15	1214.5	93.2	278	4 US-10-610-843B-2	Sequence 2, Appli
16	1212.5	93.1	239	3 US-09-880-748-2038	Sequence 2038, Ap
17	1212.5	93.1	239	4 US-10-293-418-2038	Sequence 2038, Ap
18	1210.5	92.9	280	4 US-10-611-588C-1	Sequence 1, Appli
19	1205.5	92.5	280	5 US-10-880-922-6	Sequence 6, Appli
20	1203.5	92.4	280	4 US-10-610-843B-3	Sequence 3, Appli
21	1196.5	91.8	280	5 US-10-880-922-5	Sequence 5, Appli
22	1196.5	91.8	280	5 US-10-880-922-56	Sequence 56, Appl
23	1195.5	91.7	280	5 US-10-880-922-60	Sequence 60, Appl
24	1192.5	91.5	280	5 US-10-880-922-61	Sequence 61, Appl
25	1191.5	91.4	239	3 US-09-880-748-2015	Sequence 2015, Ap
26	1191.5	91.4	239	4 US-10-293-418-2015	Sequence 2015, Ap
27	1191.5	91.4	280	5 US-10-880-922-55	Sequence 55, Appl

28	1178	90.4	244	4 US-10-322-673-42	Sequence 42, Appl
29	1178	90.4	244	5 US-10-981-465-42	Sequence 42, Appl
30	1178	90.4	244	5 US-10-981-621-42	Sequence 42, Appl
31	1178	90.4	244	5 US-10-981-673-42	Sequence 42, Appl
32	1178	90.4	244	5 US-10-981-691-42	Sequence 42, Appl
33	1178	90.4	309	4 US-10-052-798-9	Sequence 9, Appli
34	1178	90.4	309	4 US-10-288-917-9	Sequence 9, Appli
35	1178	90.4	309	4 US-10-423-448-9	Sequence 9, Appli
36	1139.5	87.5	239	3 US-09-880-748-2018	Sequence 28, Appl
37	1139.5	87.5	239	4 US-10-293-418-2018	Sequence 2018, Ap
38	1133	87.0	244	4 US-10-322-673-45	Sequence 45, Appl
39	1133	87.0	244	5 US-10-981-465-45	Sequence 45, Appl
40	1133	87.0	244	5 US-10-981-621-45	Sequence 45, Appl
41	1133	87.0	244	5 US-10-981-673-45	Sequence 45, Appl
42	1133	87.0	244	5 US-10-981-691-45	Sequence 45, Appl
43	1133	87.0	244	5 US-10-981-691-45	Sequence 45, Appl
44	1132.5	86.9	239	3 US-09-880-748-2035	Sequence 2035, Ap
45	1132.5	86.9	239	4 US-10-293-418-2035	Sequence 2035, Ap

ALIGNMENTS

RESULT 1
US-10-032-037B-204
; Sequence 204, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; CURRENT FILING DATE: 2001-12-31
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-204

Query Match	96.7%	Score	1260.5	DB 4	Length	266
Best Local Similarity	98.4%	Pred. No.	3.2e-82			
Matches	241	Conservative	0	Mismatches	3	Indels 1; Gaps 1;
QY	2	EVQLVSGGGVVRPGGSLRLSCAASGFTTDDYGMVSRVQAPGKLEWVSGINWNGGSTGY	61			
Db	23	EVQLVSGGGVVRPGGSLRLSCAASGFTTDDYGMVSRVQAPGKLEWVSGINWNGGSTGY	82			
QY	62	ADSVKGRFTISRDNAKNSLYLQNSLRAREDYAVYICARMRAPVWGQGLTVTVSRGGGS	121			
Db	83	ADSVKGRFTISRDNAKNSLYLQNSLRAREDYAVYICARMRAPVWGQGLTVTVSRGGGS	142			
QY	122	GGGGSGGGSSSELTQDPVSVVALGQTVRITCCQDSLSRSYASWYQKPGQAPVLIYGN	181			
Db	143	GGGGSGGGSSSELTQDPVSVVALGQTVRITCCQDSLSRSYASWYQKPGQAPVLIYGN	202			
QY	182	NRPSGIPDRFSGSSSGNTASLTITGAQAEADYVYCNISRDSSGNHVVFGGGLTVLGGG	241			
Db	203	NRPSGIPDRFSGSSSGNTASLTITGAQAEADYVYCNISRDSSGNHVVFGGGLTVLGGG	261			
QY	242	GCYAK 246				
Db	262	AAKAK 266				

RESULT 2
US-10-029-988B-204
; Sequence 204, Application US/10029988B
; Publication No. US20040001839A1

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; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-204

Query Match      96.7%; Score 1260.5; DB 4; Length 266;
Best Local Similarity 98.4%; Pred. No. 3.2e-82;
Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY  2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 61
DB  23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 82

QY  62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 121
DB  83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 142

QY  122 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 181
DB  143 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 202

QY  182 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGGG 241
DB  203 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGA 261

QY  242 GCKAK 246
DB  262 AAKAK 266

; RESULT 3
US-10-032-423A-204
; Sequence 204, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 204
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-204

Query Match      96.7%; Score 1260.5; DB 4; Length 266;
Best Local Similarity 98.4%; Pred. No. 3.2e-82;
Matches 241; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY  2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 61
DB  23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 82

QY  62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 121
DB  83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 142

QY  122 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 181
DB  143 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 202

QY  182 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGGG 241
DB  203 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGA 261

QY  242 GCKAK 246
DB  262 AAKAK 266

; RESULT 4
US-10-032-037B-25
; Sequence 25, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-25

Query Match      96.5%; Score 1257; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.9e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 61
DB  23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMSVVRQAPGKGLVWVSGINWNGSGTGY 82

QY  62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 121
DB  83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVIMWGQTLVTVSRGGGS 142

QY  122 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 181
DB  143 GGGSGGGGSELTDQDPAVSVALGQTVRITCGDLSRLSYASWYQKPGQAPVLIYGN 202

QY  182 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGG 239
DB  203 NRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLGG 260

; RESULT 5
US-10-029-988B-25
; Sequence 25, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25

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; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match          96.5%; Score 1257; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.9e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 61
    |||
Db  23 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 82
    |||

QY  62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 121
    |||
Db  83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 142
    |||

QY  122 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 181
    |||
Db  143 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 202
    |||

QY  182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 239
    |||
Db  203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 260
    |||

RESULT 6
US-10-032-423A-25
; Sequence 25, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-25

Query Match          96.5%; Score 1257; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.9e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 61
    |||
Db  23 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 82
    |||

QY  62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 121
    |||
Db  83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 142
    |||

QY  122 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 181
    |||
Db  143 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 202
    |||

QY  182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 239
    |||
Db  203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 260
    |||

RESULT 7
US-10-029-926B-25
; Sequence 25, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
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; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-25

Query Match          96.5%; Score 1257; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 5.9e-82;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 61
    |||
Db  23 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 82
    |||

QY  62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 121
    |||
Db  83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 142
    |||

QY  122 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 181
    |||
Db  143 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 202
    |||

QY  182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 239
    |||
Db  203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 260
    |||

RESULT 8
US-10-610-843B-1
; Sequence 1, Application US/10610843B
; Publication No. US20040202665A1
; GENERAL INFORMATION:
; APPLICANT: Lazarovits, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
; FILE REFERENCE: 10793/72
; CURRENT APPLICATION NUMBER: US/10/610,843B
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 60/393,453
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-610-843B-1

Query Match          96.2%; Score 1253; DB 4; Length 277;
Best Local Similarity 99.6%; Pred. No. 1.1e-81;
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  2 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 61
    |||
Db  23 EVQLVESGGGVVPRPGSRLRLSCAASGFTFDYGMWVRQAPGKLEWVSGINWNGSGTGY 82
    |||

QY  62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 121
    |||
Db  83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVINGOGTLVTVSRGGGS 142
    |||

QY  122 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 181
    |||
Db  143 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDSLSRYSYASWYQKPGQAPVLVIYGN 202
    |||

QY  182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYICNSRDSGNHVVFGGTKLTVLG 239
    |||
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Db 203 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 260
|||||

RESULT 9

US-10-032-037B-203
; Sequence 203, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-203

Query Match 94.6%; Score 1233; DB 4; Length 277;
Best Local Similarity 97.9%; Pred. No. 3.1e-80;
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 61
|||
Db 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 82
|||

Qy 62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVWGQGLTVTSRGGGGS 121
|||
Db 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARLTHPYFWGQGLTVTSRGGGGS 142
|||

Qy 122 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 181
|||
Db 143 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 202
|||

Qy 182 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 239
|||
Db 203 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 260
|||

RESULT 10

US-10-029-988B-203
; Sequence 203, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-203

Query Match 94.6%; Score 1233; DB 4; Length 277;
Best Local Similarity 97.9%; Pred. No. 3.1e-80;
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 61
|||

Db 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 82
|||
Qy 62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVWGQGLTVTSRGGGGS 121
|||
Db 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARLTHPYFWGQGLTVTSRGGGGS 142
|||

Qy 122 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 181
|||
Db 143 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 202
|||

Qy 182 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 239
|||
Db 203 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 260
|||

RESULT 11

US-10-032-423A-203
; Sequence 203, Application US/10032423A
; Publication No. US20040002450A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/45
; CURRENT APPLICATION NUMBER: US/10/032,423A
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-423A-203

Query Match 94.6%; Score 1233; DB 4; Length 277;
Best Local Similarity 97.9%; Pred. No. 3.1e-80;
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 61
|||
Db 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDYDGMWVRQAPGKGLVWVSGINWNGSGTGY 82
|||

Qy 62 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVWGQGLTVTSRGGGGS 121
|||
Db 83 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARLTHPYFWGQGLTVTSRGGGGS 142
|||

Qy 122 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 181
|||
Db 143 GGGSGGGGSSSELTDPAVSVVALGQTVRITCQGDLSRYSYASWYQKPGQAPVLVIYGN 202
|||

Qy 182 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 239
|||
Db 203 NRPSGIPDRFSGSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGKTLTVLG 260
|||

RESULT 12

US-10-029-926B-203
; Sequence 203, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 277

TYPE: PRT
ORGANISM: Homo sapiens
US-10-029-926d-203

Query Match 94.6%; Score 1233; DB 4; Length 277;
Best Local Similarity 97.9%; Pred. No. 3.1e-80;
Matches 233; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 61
DB 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 82

QY 62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMRAPVIMQGTTLVTVSRGGGG 121
DB 83 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARLTHPYFWQGTTLVTVSRGGGG 142

QY 122 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 181
DB 143 GGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 202

QY 182 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239
DB 203 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 260

RESULT 13
US-09-880-748-937
Sequence 937, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 937
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-937

Query Match 93.5%; Score 1218.5; DB 3; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.9e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 61
DB 1 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 60

QY 62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMR-APVIMQGTTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARRRYALDYWGQGTTLVTVSRGGG 120

QY 121 SGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 180
DB 121 SGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 180

QY 181 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239
DB 181 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239

RESULT 14
US-10-293-418-937
Sequence 937, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 937
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-937

Query Match 93.5%; Score 1218.5; DB 4; Length 239;
Best Local Similarity 97.9%; Pred. No. 2.9e-79;
Matches 234; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 61
DB 1 EVQLVESGGGVVRRPGGSLRLSCAASGFTDDYGMWVRQAPGKLEWVSGINWNGGSTGY 60

QY 62 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARMR-APVIMQGTTLVTVSRGGG 120
DB 61 ADSVKGRFTISRDNKNSLYLQWNSLRADTAIVYICARRRYALDYWGQGTTLVTVSRGGG 120

QY 121 SGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 180
DB 121 SGGSGGGGSSSELTQDPVAVSVALGQTVRITCGDLSRSYASWYQKPGQAPVLIYGN 180

QY 181 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239
DB 181 NRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239

RESULT 15
US-10-610-843B-2
Sequence 2, Application US/10610843B
Publication No. US20040202665A1
GENERAL INFORMATION:
APPLICANT: Lazarovitch, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPEUTIC TREATMENT
FILE REFERENCE: 10793/72
CURRENT APPLICATION NUMBER: US/10/610,843B
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: 60/393,453
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 278
TYPE: PRT
ORGANISM: Homo sapiens

US-10-610-843B-2

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Query Match          93.2%; Score 1214.5; DB 4; Length 278;
Best Local Similarity 97.5%; Pred. No. 6.4e-79;
Matches 233; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 2 EVQLVESGGGVVRRPGGSLRLSCAASGFTFD-DYGMWVVRQAPGKLEWVSGINWNGGSTG 60
   |||||
Db 23 EVQLVESGGGVVRRPGGSLRLSCAASGFTFDLTHPVFWVRQAPGKLEWVSGINWNGGSTG 82
   |||||

Qy 61 YADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLVTVSRGGGG 120
   |||||
Db 83 YADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARMRAPVINGQGTLVTVSRGGGG 142
   |||||

Qy 121 SGGGGSGGGSGSELTQDPAVSVALGQTVRIITCGDSLRSYYASWYQQKPGQAPVLIYVK 180
   |||||
Db 143 SGGGGSGGGSGSELTQDPAVSVALGQTVRIITCGDSLRSYYASWYQQKPGQAPVLIYVK 202
   |||||

Qy 181 NNRPSGIPDRFSGSSSGNTASLITGAQAEADYYCNSRDSSGNHVVFGGGTKLTVLG 239
   |||||
Db 203 NNRPSGIPDRFSGSSSGNTASLITGAQAEADYYCNSRDSSGNHVVFGGGTKLTVLG 261
   |||||
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Search completed: November 18, 2005, 22:17:53
Job time : 110.42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:53:49 ; Search time 3.1041 Seconds
(without alignments)
89.536 Million cell updates/sec

Title: US-10-029-926D-208
Perfect score: 1303
Sequence: 1 MEVLVSGGGVVRPGSLR.....VVFGGTKLTVLGGGCKAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pbp:
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pbp:
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pbp:
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pbp:
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pbp:
6: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pbp:
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pbp:
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pbp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	51.0	250	1	US-10-512-184-27
2	662	50.8	252	1	US-10-512-184-28
3	640	49.1	327	1	US-10-512-184-26
4	640	49.1	327	1	US-10-512-184-62
5	640	49.1	327	1	US-10-512-184-64
6	640	49.1	328	1	US-10-512-184-63
7	640	49.1	576	1	US-10-512-184-65
8	640	49.1	625	1	US-10-512-184-47
9	636.5	48.8	261	1	US-10-512-184-35
10	636.5	48.8	313	1	US-10-512-184-72
11	630.5	48.4	263	1	US-10-512-184-29
12	614.5	47.2	259	1	US-10-512-184-31
13	614.5	47.2	329	1	US-10-512-184-68
14	603.5	46.3	329	1	US-10-512-184-33
15	603.5	46.3	329	1	US-10-512-184-70
16	596	45.7	251	1	US-10-512-184-30
17	596	45.7	320	1	US-10-512-184-67
18	596	45.7	569	1	US-10-512-184-66
19	596	45.7	618	1	US-10-512-184-48
20	595	45.7	543	1	US-10-485-664-3
21	586	45.0	269	1	US-10-839-799-109
22	540.5	41.5	248	1	US-10-512-184-32
23	540.5	41.5	317	1	US-10-512-184-69
24	524	40.2	259	1	US-10-512-184-34
25	524	40.2	371	1	US-10-512-184-71

26	524	40.2	626	1	US-10-512-184-49	Sequence 49, Appl
27	490.5	37.6	444	7	US-11-172-320-6	Sequence 6, Appl
28	488.5	37.5	122	7	US-11-144-248-24	Sequence 24, Appl
29	484	37.1	470	7	US-11-144-248-46	Sequence 46, Appl
30	478.5	36.7	473	7	US-11-144-248-50	Sequence 50, Appl
31	478	36.7	121	1	US-10-789-273-9	Sequence 9, Appl
32	473	36.3	138	1	US-10-789-273-8	Sequence 8, Appl
33	473	36.3	470	7	US-11-144-248-49	Sequence 49, Appl
34	472.5	36.3	248	1	US-10-512-184-36	Sequence 36, Appl
35	472.5	36.3	615	1	US-10-512-184-50	Sequence 50, Appl
36	470	36.1	135	7	US-10-789-273-12	Sequence 12, Appl
37	469	36.0	125	7	US-11-144-248-16	Sequence 16, Appl
38	467.5	35.9	139	1	US-10-721-763-33	Sequence 33, Appl
39	465	35.7	470	7	US-11-144-248-45	Sequence 45, Appl
40	451	34.6	124	7	US-11-144-248-8	Sequence 8, Appl
41	446	34.2	98	1	US-10-789-273-10	Sequence 10, Appl
42	446	34.2	98	7	US-11-144-248-32	Sequence 32, Appl
43	439	33.7	98	7	US-11-144-248-30	Sequence 30, Appl
44	423	32.5	121	7	US-11-077-978-2	Sequence 2, Appl
45	420.5	32.3	120	7	US-11-077-978-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581, 01US01
; CURRENT APPLICATION NUMBER: US/10/512, 184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match	51.0%;	Score 664;	DB 1;	Length 250;
Best Local Similarity	58.1%;	Pred. No. 2.1e-27;		
Matches 144;	Conservative 24;	Mismatches 66;	Indels 14;	Gaps 6;
QY	3	VQLVESGGGVVRPGGSLRLSCAASGFTFDY	GNSVWRQAPGKLEWVSGINWNGSGTGYA	62
Db	4	VTLDSEGGGLQTPEDGSLVCKASGFTFSNGMAVWRQAPGKLEWVAGIDGSGFTGYG	63	
QY	63	DSVKGRTISRDNAKNSLYLQMNLSRAEDTAVYVCARMRAPV-----	INGQGTTLVTISR	116
Db	64	AAVKGRTISRDNGQSTVRLQLNLSRAEDTAVYCARGTGCGGDDRIDAWGHGTEVTSS	123	
QY	117	GG-GSGGGGGGGGGG---GSSSELTQDPASVVALGQTVRITCGDPSLSRYASWYQOK-PQG	171	
Db	124	GSTSGSGKPGPGSGSTKGAPALQPSVSSANLGGTVKITCSGST--AHY-SHWQOKSPGS	180	
QY	172	APVLVYGNKRNPSGIPDRPFGSSSGSSNTASLTITGAQAEADYYCNRSRDSNGHVVFGG	231	
Db	181	APVTLISFNQRPDIPSPRPSFGSGSGSTGLTITGVRAEDEAVYVCGGWDRTSITAGLFGA	240	
QY	232	GTKLTVLG	239	
Db	241	GTTLTVLG	248	

US-10-512-184-63

Query Match 49.1%; Score 640; DB 1; Length 327;
Best Local Similarity 55.0%; Pred. No. 3.5e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 327
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising lactoferricin - linker -
OTHER INFORMATION: scFv CWP22.
US-10-512-184-64

Query Match 49.1%; Score 640; DB 1; Length 327;
Best Local Similarity 55.0%; Pred. No. 3.5e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 328
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising RS - linker -
OTHER INFORMATION: scFv CWP22.

Query Match 49.1%; Score 640; DB 1; Length 576;
Best Local Similarity 55.0%; Pred. No. 5e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 328
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising RS - linker -
OTHER INFORMATION: scFv CWP22.

US-10-512-184-63

Query Match 49.1%; Score 640; DB 1; Length 328;
Best Local Similarity 55.0%; Pred. No. 3.6e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 576
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising chitinase - linker -
OTHER INFORMATION: scFv CWP22.
US-10-512-184-65

US-10-512-184-65

Query Match 49.1%; Score 640; DB 1; Length 576;
Best Local Similarity 55.0%; Pred. No. 5e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
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US-10-512-184-65

US-10-512-184-65

Query Match 49.1%; Score 640; DB 1; Length 576;
Best Local Similarity 55.0%; Pred. No. 5e-26;
Matches 142; Conservative 23; Mismatches 67; Indels 26; Gaps 8;
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 576
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising chitinase - linker -
OTHER INFORMATION: scFv CWP22.
US-10-512-184-65


```
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match          47.2%; Score 614.5; DB 1; Length 259;
Best Local Similarity 49.8%; Pred. No. 5.2e-25;
Matches 124; Conservative 43; Mismatches 67; Indels 15; Gaps 6;

QY 2 EVLVESGGVVRPGGSLRLSCAASGFTPDYDGMVSRVQAPGKGLWVSGINWNGSGTGY 61
Db 3 EVKLESGLPKPGETVKISKASGYFTFYGNVWVQAPGKGLKMGWINTYTGPTY 62
QY 62 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCARMRA-PV-----IWGGTFLVTISR 116
Db 63 ADDFKGRFAFSLSTSTSTAFQLNNLNKEDTATYFCARYGNPYTMDYWGQGTSLTVSS 122
QY 117 GGGGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRTICQDLSRSY-----YASWYQOK 168
Db 123 GGGGGGGGGGGGGSDIVLSQSPSLAVSVGKVTMSCKSSQSLLYSSNQKNYLAITYQOK 182
QY 169 PGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRDSGNHV 228
Db 183 PQGSPKLLIYWASTRESGVDRFTGSGSGTDFLTITSSVKAEDLAVYICQOYYS--YPFT 240
QY 229 FGGGTGLTV 237
Db 241 FGSGTGLKLEI 249

RESULT 13
US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match          47.2%; Score 614.5; DB 1; Length 329;
Best Local Similarity 49.8%; Pred. No. 6e-25;
Matches 124; Conservative 43; Mismatches 67; Indels 15; Gaps 6;

QY 2 EVLVESGGVVRPGGSLRLSCAASGFTPDYDGMVSRVQAPGKGLWVSGINWNGSGTGY 61
Db 73 EVKLESGLPKPGETVKISKASGYFTFYGNVWVQAPGKGLKMGWINTYTGPTY 132
QY 62 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCARMRA-PV-----IWGGTFLVTISR 116
Db 133 ADDFKGRFAFSLSTSTSTAFQLNNLNKEDTATYFCARYGNPYTMDYWGQGTSLTVSS 192
QY 117 GGGGGGGGGGGGGSS-ELTQDP-AVSVALGQTVRTICQDLSRSY-----YASWYQOK 168
Db 193 GGGGGGGGGGGGGSDIVLSQSPSLAVSVGKVTMSCKSSQSLLYSSNQKNYLAITYQOK 252
QY 169 PGQAPVLVIYGNKRNPSGIPDRFSGSSSGNTASLTITGAQAEDEADYICNSRDSGNHV 228
Db 253 PQGSPKLLIYWASTRESGVDRFTGSGSGTDFLTITSSVKAEDLAVYICQOYYS--YPFT 310
QY 229 FGGGTGLTV 237

; OTHER INFORMATION: Description of Artificial Sequence: scFv VDCw with
```

```
Db          311 FGSQTKLEI 319
||| ||| :
; OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-70
Query Match          46.3%; Score 603.5; DB 1; Length 329;
Best Local Similarity 49.4%; Pred. No. 1.7e-24;
Matches 123; Conservative 42; Mismatches 69; Indels 15; Gaps 6;
GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-33
Query Match          46.3%; Score 603.5; DB 1; Length 259;
Best Local Similarity 49.4%; Pred. No. 1.7e-24;
Matches 123; Conservative 42; Mismatches 69; Indels 15; Gaps 6;
GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-70
Query Match          46.3%; Score 603.5; DB 1; Length 329;
Best Local Similarity 49.4%; Pred. No. 1.7e-24;
Matches 123; Conservative 42; Mismatches 69; Indels 15; Gaps 6;
GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 70
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
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Search completed: November 18, 2005, 22:18:08
Job time : 4.1041 secs

Search completed: November 18, 2005, 22:18:08
Job time : 4.1041 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2005, 21:35:01 ; Search time 24.0568 Seconds
(without alignments)
983.894 Million cell updates/sec

Title: US-10-029-926D-208
Perfect score: 1303
Sequence: 1 MEVQLVESGGGVVRPGSLR.....VVFGGTKLTVLGGGCKRAK 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	44.3	268	2 A56446	Ig heavy chain V r
2	568	43.6	109	2 S19663	Ig lambda chain V
3	562	43.1	108	2 S47184	Ig lambda chain -
4	561.5	43.1	249	2 S41374	single chain Fv an
5	551.5	42.3	110	2 S36272	Ig lambda chain V
6	546	41.9	127	2 S70444	Ig lambda chain pr
7	541	41.5	108	2 S38498	Ig lambda chain -
8	539	41.4	109	2 S38496	Ig lambda chain -
9	530	40.7	233	2 S25748	Ig lambda chain V-
10	527	40.4	108	1 L3HUSH	Ig lambda chain V-
11	522.5	40.1	233	2 JC5322	p53 specific singl
12	518.5	39.8	110	2 S19672	Ig lambda chain V-
13	517.5	39.7	146	2 S02083	Ig lambda chain V-
14	513	39.4	98	2 S26928	Ig heavy chain V r
15	510.5	39.2	128	2 S31595	Ig heavy chain V r
16	503	38.6	95	2 S36060	Ig lambda chain -
17	503	38.6	115	2 S31726	Ig lambda chain V
18	503	38.6	121	2 S31118	Ig heavy chain - h
19	502	38.5	123	2 S30532	Ig heavy chain V r
20	502	38.5	233	2 S25741	Ig lambda chain -
21	501	38.4	121	2 S31104	Ig heavy chain (su
22	495.5	38.0	112	2 PH1654	Ig heavy chain V r
23	491	37.7	120	2 S36273	Ig heavy chain V r
24	488	37.5	134	2 S31699	Ig heavy chain V r
25	487	37.4	138	2 S31666	Ig heavy chain V-D
26	485.5	37.3	120	2 S44111	Ig heavy chain V-D
27	485.5	37.3	145	2 S11239	Ig heavy chain - h
28	485	37.2	119	2 S31108	Ig heavy chain - h
29	485	37.2	160	2 S05271	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TAN>

A:Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 44.3%; Score 577; DB 2; Length 268;

Best Local Similarity 50.2%; Pred. No. 7.2e-33;

Matches 121; Conservative 34; Mismatches 78; Indels 8; Gaps 5;

QY	2	EVLVESGGGVVRPGSLRLSCAASGFTFDYQMSVVRQAPGKGLVWVSINWNGSGTGY	61
DB	3	QVKQLQSGAELVKPGASVKLSCTTSCTGFKIKDTYMHVVKRPEQGLEWIGRIAPANGITKY	62
QY	62	ADSVKGRFTISRDNAKNSLYLQNSLRAREDTAVYVCAR---WEAPVTWGQGLTVTVSRGG	118
DB	63	DKRFQKATIAADTSSNTAYLQLSLTSEDYAVYVCASYLYLTRENYWGQGLTVTVSSGG	122
QY	119	GGSGGGGGGGSS-ELTDPAV-SVALGQTVRITCGDSLRSYASWYQQKPGQAPVLV	176
DB	123	GGSGGGGGGGGGGDIETLQSPAINASLGEKVTMSCEASSVN-FIYWIQKSDASPKLW	181
QY	177	IYKNNRPSGIPDRFSGSSSGNTASLTITCAQAEADYVYCNDRDSSGNHVFGGGTKLT	236
DB	182	VYITSHLPVGPVRFSGSGSNSYSLTISSEGEADAATYICQQFTSS--PFTFGSGTKLE	239
QY	237	V 237	
DB	240	I 240	

RESULT 2

S19663

Ig lambda chain V region (clone alpha-BSA3) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19663

R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter

J. Mol. Biol. 222, 581-597, 1991

A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on p

A:Reference number: S19663; MUID:92085276; PMID:1748994

A;Accession: S19663
A;Molecule type: mRNA
A;Residues: 1-109 <MAR>
A;Cross-references: UNIPARC:UPI000039C3B; EMBL:X61640; NID:G29492; PIDN:CAA43821.1; PID
C;Species: Homo sapiens (man)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.6%; Score 568; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 190
Db 1 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 60

Qy 191 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 239
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVLG 109

RESULT 3

S47184

Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A;Reference number: S47184
A;Accession: S47184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MC>
A;Cross-references: UNIPARC:UPI0000031AF6; EMBL:X79783; NID:G506426; PIDN:CAA56179.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 562; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e-32;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 190
Db 1 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 60

Qy 191 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVL 238
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVVFGGTKLTVL 108

RESULT 4

S41374

single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antibody
A;Reference number: S41374
A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 43.1%; Score 561.5; DB 2; Length 249;
Best Local Similarity 48.6%; Pred. No. 7.8e-32;
Matches 121; Conservative 36; Mismatches 71; Indels 21; Gaps 6;

Qy 2 EVQLVESGGGVVPRPGGSLRLSQAASGFTFDYGMNWVRQAPKGLVWVSGINMGSGTGY 61
Db 1 QVQLQQSGAELVRPGASVKLSCTASGFNFKDDYTHWVKQRPEKGLWIARAPASGNVYK 60
Qy 62 ADSVKGRTTISRDNKNSLYLOMNSLRAREDPAVYCAR---MRAPVINGGTLVTYVRG 117
Db 61 VPRFDKATITADTSSNTAYLLLSLTSEDPAVYCARRDPLTYSLVGWMGGSTVTYSSR 120
Qy 118 GGSGGGGGGGGSS-ELTQD-PAVSVALGQTVRITCQ-----GDSLSRSYASWYQ 166
Db 121 GGSGGGGGGGGGGDIETQSPSPVVPVPGESVISCSSKSLYSDDGS---YLFWFL 176
Qy 167 KPGQAPVLVIYKKNRPSGIPDRFSGSSSNTASLTITGAQAEADYYCNSRDSSGNH 226
Db 177 QRPQSPQLLYIRMSNLASGVDPDRFSGSGSGTFTLRISRVEARDVGVVYCMQHRE--YP 234
Qy 227 VVFGGTKL 235
Db 235 LTFGAGTKL 243

RESULT 5

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36272
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36272
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-110 <GR>
A;Cross-references: UNIPARC:UPI0000118DF6; EMBL:Z18833; NID:G33419; PIDN:CAA79285.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 551.5; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.6e-31;
Matches 108; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 131 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 190
Db 1 SSELTPDPAVSVALGQTVRITTCQDLSRSYASWYQKPGQAPVLVIYKKNRPSGIPDR 60

Qy 191 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGN-HVFGGTKLTVLG 239
Db 61 FSGSSSGNTASLTITGAQAEADYYCNSRDSSGNLVVFGGTKLTVLG 110

RESULT 6

S70444

Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004
C;Accession: S70444; S70426
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of f
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <CU>
A;Cross-references: UNIPROT:Q9NSD6; UNIPARC:UPI0000176807
A;Experimental source: clone E29.1
R;Tonnelle, C.
submitted to the EMBL Data Library, May 1990
A;Reference number: S70426
A;Accession: S70426

A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate to form a tetramer with four identical chain disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:Keywords: immunoglobulin homology <IMM>
F:14-88/Domain: immunoglobulin homology
F:21-86/Disulfide bonds: #status experimental
Query Match 40.4%; Score 527; DB 1; Length 108;

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RESIT.T 2

1	QVKLQSGPELKPKGETVKISKASGYTFDYGMNWKQAPGRGLKMGWINTYTGEPY	60
62	ADSVKGRFTISRDNAKNSLYLQWNSLRAREDATVYYCAR--MEAPVWGOGTLVTVSRGG	118
61	ADDFKGRFAPSLTSGASTAYLQINNKNEDATYFCARKDLLAYFDYWGOGTTVTVSSGG	120
119	GGSGGGGGGGGSS--ELTODP-AVSVALGOTVIRITCGDSLRYSYASWYQOKFGQAP---	173
121	GGSGGGGGGGGGDIELTQSPSLSASLGGKVTITCKASQDINKYIATWYQHKPGKGRSA	180
174	-VLVTYVGKNRPSGIPDRFGSGSSGNTASLITITGAQAEDEADYVCNRSRDSGHNHVFGGG	232
181	HTLHYIQ-----PGIPSRFSGSGGRDYFSISNLEPEDIATYYCLHYD---NLHTFGGG	233
233	TKL	235
234	TKL	236

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RESULT 6
Q7TQM2_MOUSE
ID Q7TQM2_MOUSE PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SCFv 6H8 protein (Fragment).
OS Name=scfv 6H8;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/C;
RC MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Effekhari P., Billiard P., Wallukat G., Hoebeke J.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAF00495.1; -; Genomic_DNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q7TQM2; 1-236.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 2_v.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR NON_TER
SQ SEQUENCE 243 AA; 25976 MW; BEFF664D5DCF4F76 CRC64;

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[illegible]

2

Db 138 GGGGGGGGSRQMTQSPASLSVSGELVITTCRASENIYSNLAWYQQKGRSPQLLVTA 197
QY 180 KNNRPSGIPDRFGSSGNTASITITGAQAEADYYCNSRDSGSHVFGGTTKLTIV 237
Db 198 ATNLADGVSRFGSGGSGTQYSLKINSLOSEDFGSYYC--QHPWGTPYTFGGGTRLEI 253

RESULT 10
Q6GMW4 HUMAN
ID Q6GMW4 HUMAN PRELIMINARY; PRT; 233 AA.
AC Q6GMW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]

NUCLEOTIDE SEQUENCE.
TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073786; AAH73786.1; -, mRNA.
DR SMR; Q6GMW4; 23-229.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein
SQ SEQUENCE 233 AA; 24855 MW; 4626773B8FDE5BD CRC64;
Query Match 40.7%; Score 530; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 2e-31;
Matches 100; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 131 SSELTPDPAVSVALGQTVRITTCQGDSLSRYASVYQKPGQAPVLVIYKNNRPSGIPDR 190

Db 20 SSELTPDPAVSVALGQTVRITTCQGDSLSRYASVYQKPGQAPVLVIYKNNRPSGIPDR 79
QY 191 FSGSSGNTASITITGAQAEADYYCNSRDSGSHVFGGTTKLTIVLG 239
Db 80 FSGSSGNTASITITGAQAEADYYCNSRDSGSHVFGGTTKLTIVLG 128

RESULT 11
LV3A HUMAN
ID LV3A HUMAN STANDARD; PRT; 108 AA.
AC F01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN PROTEIN SEQUENCE.
RP MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges";
RL J. Biol. Chem. 245:2171-2176 (1970).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A01980; L3HUSH.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 97 Ig-like.
FT DISULFID 21 86
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11393 MW; E7E1229586411A56 CRC64;
Query Match 40.4%; Score 527; DB 1; Length 108;
Best Local Similarity 92.6%; Pred. No. 1.4e-31;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 132 SELTPDPAVSVALGQTVRITTCQGDSLSRYASVYQKPGQAPVLVIYKNNRPSGIPDRF 191
Db 1 SELTPDPAVSVALGQTVRITTCQGDSLSRGYDAVYQKPGQAPVLVIYGRNNRPSGIPDRF 60
QY 192 SGSSSGNTASITITGAQAEADYYCNSRDSGSHVFGGTTKLTIVLG 239
Db 61 SGSSSGHTASITITGAQAEADYYCNSRDSGSHVFGGTTKLTIVLG 108
RESULT 12
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

```

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686p15220.
GN Name=DKFZp686p15220;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Meves H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSPF; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 39.3%; Score 512; DB 2; Length 472;
Best Local Similarity 48.5%; Pred. No. 9.7e-30;
Matches 114; Conservative 19; Mismatches 70; Indels 32; Gaps 5;

QY 2 EVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMVSWVRAQPGKLEWVSGINWNGSGTGY 61
Db 20 EVQLVESGGGLVQPGSLRLSCAASGFTFDYAMHWVRAQPGKLEWVSGINWNGSIAT 79

QY 62 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCAR-----MRAPVWGQGLTAVT 113
Db 80 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCAKEIGHNPFYYGMVDMVGQGTITV 139

QY 114 VSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 173
Db 140 VS-----SASTKGSVPLAPSSKTSKGTALGC---LVKDYFPE-----P 178

QY 174 VLVIYKKNRPSGI---PDRFGSSSGNTASLTITGAQAEADYVYCNRSRDSGN 225
Db 179 VTVSNNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTICNVNHPKSN 233

RESULT 13
QN5K4 HUMAN
ID QN5K4 HUMAN PRELIMINARY; PRT; 499 AA.
AC QN5K4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC37165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield F.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032249; AAH32249.1; -; mRNA.
DR HSPF; P01876; IOW0.
DR SMR; Q8N5K4; 269-477.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 499 AA; 53376 MW; 93ASC89582054F32 CRC64;

Query Match 39.1%; Score 510; DB 2; Length 499;
Best Local Similarity 51.3%; Pred. No. 1.5e-29;
Matches 120; Conservative 14; Mismatches 42; Indels 58; Gaps 8;

QY 2 EVQLVESGGGVVRRPGSLRLSCAASGFTFDYGMVSWVRAQPGKLEWVSGINWNGSGTGY 61
Db 20 EVQLVESGGGVVRRPGSLRLSCATSGFTFDGSGASVWRAQPGKLEWVSSINWNGSTNY 79

QY 62 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCARMAPV-----IWQGG 109
Db 80 ADSVKGRFTISRDNKNSLYLQMSLRADTAIVYCARDPTKYCGSGCLGYVMDVWKG 139

QY 110 TLVTVSRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 162
Db 140 TTVTVS-----SASPTSPKVPPLSLCSTQPDGNVVIACLVGG----- 176

QY 163 SWYQOKP-----GQAPVLVIYKKNRPSGIPDRFGSSSGNTASLTITGAQ 208
Db 177 -FFPQEPPLSVTWSSGQG-----VTARNFPFPG---QDASGDLYTTSQTLPATQ 222

RESULT 14
Q569F4 HUMAN
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 39.0%; Score 508.5; DB 2; Length 469;
Best Local Similarity 50.0%; Pred. No. 1.8e-29; Indels 29; Gaps 5;
Matches 116; Conservative 18; Mismatches 69;
QY 2 EVLVESGGVVRPG4SLRLSCAASGFTFDYGMVWRQAPGKLEWVGINWGGSTGY 61
DB 20 EVLVESGGVVVQPGGSLRLSCAASGFTFDYAMHWVRQAPGKLEWVLSLWDGGSTY 79
QY 62 ADSVKGRFTISRDNKNSLYQNSLRAEDTAVYICARMAPV-----IWQGTLYTVSR 116
DB 80 ADSVKGRFTISRDNKNSLYQNSLRAEDTALYICATRGYSTAGFDYWGQGLTVTS- 138
QY 117 GGGGGGGGGGGSSSLTQDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLV 176
DB 139 -----SASTKGPVSFPLAPSKTSGGTALGC---LVKDYFPE-----PVTV 178
QY 177 IYGNKNNRPSGI---PDRFGSSSGNTASLTITGAQAEDADYYCNSRDSSGN 225
DB 179 SWNSGALTSGVHTFPVAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHKPSN 230

RESULT 15
QSNV73 HUMAN
ID QSNV73 HUMAN PRELIMINARY; PRT; 97 AA.
AC QSNV73;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE V2-13 protein (Fragment).
GN Name=V2-13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9728902; PubMed=9074928;
RA Kawasaki K., Minoshima S., Nakato E., Shibuya K., Shintani A.,
RA Schmeits J.L., Wang J., Shimizu N.;
RT "One-megabase sequence analysis of the human immunoglobulin lambda
RT gene locus.";
RL Genome Res. 7:250-261(1997).

DR EMBL; D87007; BAA20895.1; -; Genomic_DNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1_1
FT NON_TER 97_97
SQ SEQUENCE 97 AA; 10364 MW; 4074456BA1216B77 CRC64;
Query Match 38.7%; Score 504; DB 2; Length 97;
Best Local Similarity 99.0%; Pred. No. 6.1e-30;
Matches 96; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 131 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVYGNKNNRPSGI 190
DB 1 SSELTDPAVSVALGQTVRITCGDSLRSYASWYQKPGQAPVLVYGNKNNRPSGI 60
QY 191 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHV 227
DB 61 FSGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHL 97

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Job time : 141.461 secs

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